

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:10 ; Search time 32.5277 Seconds  
(without alignments)  
1284.140 Million cell updates/sec

**Title:** US-10-089-500-10

Perfect score: 574

Sequence: 1 DIQMTQSPSSLASVGDRVT.....HQYSKLPWTFGQGTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381

Total number of hits satisfying chosen parameter

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 03

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A Geneseq 16Dec04:\*

1: \_ geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp20018:\*

5: geneseqp2002s:\*  
6: geneseqp2002s:\*

6: [genesetp2003a8:\\*](#)

7: [genevex200308:](#)

[illegible]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	574	100.0	108	4	AA881986	AA881986 Gangliosi
2	571	99.5	128	4	AA881986	AA881986 Gangliosi
3	570	99.3	128	4	AA881993	AA881993 Gangliosi
4	564	98.3	128	4	AA881997	AA881997 Gangliosi
5	561	97.7	128	4	AA881995	AA881995 Gangliosi
6	558	97.2	128	4	AA881994	AA881994 Gangliosi
7	558	97.2	128	4	AA881992	AA881992 Gangliosi
8	557	97.0	108	6	ABU10111	ABU10111 Modified
9	548	95.5	108	4	AA881988	AA881988 Gangliosi
10	548	95.5	128	4	AA881999	AA881999 Gangliosi
11	548	95.5	128	4	AA881998	AA881998 Gangliosi
12	533	92.9	110	2	AAW70673	AAW70673 Anti-VEGF
13	533	92.9	110	5	ABP61242	ABP61242 Humanised
14	533	92.9	237	2	AAW70703	AAW70703 Protein e
15	533	92.9	650	5	ABP61241	ABP61241 Phage-di
16	531	92.5	107	2	AAW86805	AAW86805 Variable
17	531	92.5	107	2	AAW70625	AAW70625 Humanised
18	531	92.5	107	5	ABP61194	ABP61194 Humanised
19	530	92.3	110	2	AAW70675	AAW70675 Anti-VEGF
20	530	92.3	110	5	ABP61244	ABP61244 Humanised
21	529	92.2	108	2	AAW70618	AAW70618 Anti-VEGF
22	529	92.2	108	5	ABP61187	ABP61187 Humanised
23	529	92.2	108	8	ADG31782	ADG31782 V(L) doma
24	529	92.2	108	8	ADG31768	ADG31768 V(L) doma
25	529	92.2	108	8	ADG31893	ADG31893 V(L) prot

99 501 87.3 109 5 AAU74544 Human sub  
100 501 87.3 110 5 AAE28149 Human con

## ALIGNMENTS

## RESULT 1

AA81986  
ID AAB81986 standard; protein; 108 AA.

XX AC AAB81986;

DT 03-JUL-2001 (first entry)

XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 10.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.

XX Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

DR WPI; 2001-266143/27.

XX New human type complementation-determining region-transplanted antibody

PT and derivatives against ganglioside GD3, useful in diagnosis and therapy

PT of e.g. tumors, with low antigenicity, little side effects but potent

PT activity in cancer.

XX Example 1; Page 143-144; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react

CC specifically with ganglioside GD3. The antibody and its derivatives are

CC useful in the diagnosis and therapy of tumors, particularly cancer

CC diagnosis. The present sequence is a protein used in the exemplification

CC of the invention

XX Sequence 108 AA;

Query Match 100.0%; Score 574; DB 4; Length 108;

Best Local Similarity 100.0%; Pred. No. 1.3e-34;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQQKPGKAPKLLIFYSNLSHGVPVS 60

DB 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQQKPGKAPKLLIFYSNLSHGVPVS 60

QY 61 RFSGGSGTDYTLTITSSLPEDFATYCHQYSKLPWTFGQGTKEIKR 108

DB 61 RFSGGSGTDYTLTITSSLPEDFATYCHQYSKLPWTFGQGTKEIKR 108

RESULT 2

AA81996

ID AAB81996 standard; protein; 128 AA.

XX AC AAB81996;

DT 03-JUL-2001 (first entry)

XX Ganglioside GD3 specific antibody related protein #2.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.

XX Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

PR Ganglioside GD3 specific antibody related protein #5.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.

XX Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

PR Ganglioside GD3 specific antibody related protein #5.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.

XX Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

PR Ganglioside GD3 specific antibody related protein #5.

DE Ganglioside GD3 specific antibody related protein #5.  
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX Synthetic.  
XX WO200123432-A1.  
PN 05-APR-2001.  
XX 29-SEP-2000; 2000WO-JP006774.  
PR 30-SEP-1999; 99JP-00278291.  
PR 06-APR-2000; 2000JP-00105088.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
PA Hanai N, Shitara K, Nakamura K, Niwa R;  
PI WPI; 2001-266143/27.  
DR N-PSDB; AAF86904.  
XX New human type complementation-determining region-transplanted antibody

PT and derivatives against ganglioside GD3, useful in diagnosis and therapy

PT of e.g. tumors, with low antigenicity, little side effects but potent

PT activity in cancer.

XX Example 1; Page 159-160; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react

CC specifically with ganglioside GD3. The antibody and its derivatives are

CC useful in the diagnosis and therapy of tumors, particularly cancer

CC diagnosis. The present sequence is a protein used in the exemplification

CC of the invention

XX Sequence 128 AA;

Query Match 99.5%; Score 571; DB 4; Length 128;

Best Local Similarity 99.1%; Pred. No. 2.5e-34;

Matches 107; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQQKPGKAPKLLIFYSNLSHGVPVS 60

DB 21 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQQKPGKAPKLLIFYSNLSHGVPVS 80

QY 61 RFSGGSGTDYTLTITSSLPEDFATYCHQYSKLPWTFGQGTKEIKR 108

DB 81 RFSGGSGTDYTLTITSSLPEDFATYCHQYSKLPWTFGQGTKEIKR 128

RESULT 3

AA81993

ID AAB81993 standard; protein; 128 AA.

XX AC AAB81993;

DT 03-JUL-2001 (first entry)

XX Ganglioside GD3 specific antibody related protein #2.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.

XX Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

PR Ganglioside GD3 specific antibody related protein #5.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.

XX Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

PR Ganglioside GD3 specific antibody related protein #5.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.

XX Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

PR Ganglioside GD3 specific antibody related protein #5.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.

XX Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

PR Ganglioside GD3 specific antibody related protein #5.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.

XX Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

PR Ganglioside GD3 specific antibody related protein #5.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.

XX Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

PR Ganglioside GD3 specific antibody related protein #5.



```

PR 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX WPI; 2001-266143/27.
XX
XX N-PSDB; AAF86895.
XX
XX
XX New human type complementation-determining region-transplanted antibody
XX and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.
XX
XX Example 1; Page 153; 183pp; Japanese.
XX
XX The present invention describes a monoclonal antibody which can react
XX specifically with ganglioside GD3. The antibody and its derivatives are
XX useful in the diagnosis and therapy of tumors, particularly cancer
XX diagnosis. The present sequence is a protein used in the exemplification
XX of the invention
XX
XX Sequence 128 AA;
XX
XX Query Match 99.3%; Score 570; DB 4; Length 128;
XX Best Local Similarity 99.1%; Pred. No. 3e-34;
XX Matches 107; Conservative 1; Mismatches 0; Indels 0; Gaps 0
XX
XX QY 1 DIQMTSPSSLSASVGDRTVITCSASQDISNLYNWYQOKPGKAPKLLIFYSSNLHSGVPS 60
XX |||||
XX DB 21 DIQMTSPSSLSASVGDRTVITCSASQDISNLYNWYQOKPGKAPKLLIFYSSNLHSGVPS 80
XX |||||
XX QY 61 RFSGGSGGTDYTLTIISSLOPEPATYVCHQYSKLPMTFGQGTKEIKR 108
XX |||||
XX DB 81 RFSGGSGGTDYTLTIISSLOPEPATYVCHQYSKLPMTFGQGTKEIKR 128
XX |||||
XX
XX RESULT 4
XX AAB81997
XX ID AAB81997 standard; protein; 128 AA.
XX
XX AC AAB81997;
XX
XX DT 03-JUL-2001 (first entry)
XX
XX DE Ganglioside GD3 specific antibody related protein #6.
XX
XX KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX
XX OS Synthetic.
XX
XX OS
XX
XX PN WO200123432-A1.
XX
XX PD 05-APR-2001.
XX
XX PF 29-SEP-2000; 2000WO-JP006774.
XX
XX PR 30-SEP-1999; 99JP-00278291.
XX
XX PR 06-APR-2000; 2000JP-00105088.
XX
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX WPI; 2001-266143/27.
XX
XX N-PSDB; AAF86907.
XX
XX
XX New human type complementation-determining region-transplanted antibody
XX and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.
XX

```

PS Example 1; Page 161-162; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react

CC specifically with ganglioside GD3. The antibody and its derivatives are

CC useful in the diagnosis and therapy of tumours, particularly cancer

CC diagnosis. The present sequence is a protein used in the exemplification

CC of the invention

XX

XX Sequence 128 AA;

XX

Query Match 98.3%; Score 564; DB 4; Length 128;

Best Local Similarity 98.1%; Pred. No. 8.2e-34;

Matches 106; Conservative 1; Mismatches 1; Indels 0; Gaps

QY 1 DIQMTQSPSSLSASVCDRTITCSASQDISNYLNYYQKPGKAPKLLIFYSNLSHSGVPS 60

DB 21 DIQMTQSPSSLSASVCDRTITCSASQDISNYLNYYQKPGKAPKLLIFYSNLSHSGVPS 80

QY 61 RFSGGSGGTDYTLTITSSLOPEDPATYVCHQYSKLPWTFCGGTKVEIKR 108

DB 81 RFSGGSGGTDYTLTITSSLOPEDPATYVCHQYSKLPWTFCGGTKVEIKR 128

XX

RESULT 5

AAB81995

ID AAB81995 standard; protein; 128 AA.

XX

AC AAB81995;

XX

DT 03-JUL-2001 (first entry)

XX

DE Ganglioside GD3 specific antibody related protein #4.

XX

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.

XX

OS Synthetic.

XX

XX WO200123432-A1.

XX

PD 05-APR-2001.

XX

PF 29-SEP-2000; 2000WO-JP006774.

XX

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

XX

PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX

PI Hanai N, Shitara K, Nakamura K, Niwa R;

XX

DR WPI; 2001-266143/27.

DR N-PSDB; AAF86901.

XX

XX New human type complementation-determining region-transplanted antibody

PT and derivatives against ganglioside GD3, useful in diagnosis and therapy

PT of e.g. tumors, with low antigenicity, little side effects but potent

PT activity in cancer.

XX

XX Example 1; Page 157-158; 183pp; Japanese.

XX

XX The present invention describes a monoclonal antibody which can react

CC specifically with ganglioside GD3. The antibody and its derivatives are

CC useful in the diagnosis and therapy of tumours, particularly cancer

CC diagnosis. The present sequence is a protein used in the exemplification

CC of the invention

XX

XX Sequence 128 AA;

XX

Query Match	97.7%	Score 561;	DB 4;	Length 128;
Best Local Similarity	97.2%	Pred. No. 1.3e-33;		
Matches 105; Conservative	2;	Mismatches 1;	Indels 0;	Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60  
Db |||||  
QY 21 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 80  
61 RFSGGSGGTDYTLTITSSLPQDFATYCHQYSKLPWTFCQGTKEIKR 108  
Db |||||  
81 RFSGGSGGTDYSLTITSLQPEDATYCHQYSKLPWTFCQGTKEIKR 128

RESULT 6  
AAB81994  
ID AAB81994 standard; protein; 128 AA.  
XX  
AC AAB81994;  
XX  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD3 specific antibody related protein #3.  
XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
XX  
OS Synthetic.  
XX  
PN WO200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
XX  
PR 30-SEP-1999; 99JP-00278291.  
XX  
PR 06-APR-2000; 2000JP-00105088.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
DR WPI; 2001-266143/27.  
XX  
DR N-PSDB; AAF86898.  
XX  
New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX  
PS Example 1; Page 155-156; 183pp; Japanese.  
XX  
The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumours, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX  
SQ Sequence 128 AA;

Query Match 97.2%; Score 558; DB 4; Length 128;  
Best Local Similarity 98.1%; Pred. No. 2.2e-33;  
Matches 106; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60  
Db |||||  
QY 21 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 80  
61 RFSGGSGGTDYTLTITSSLPQDFATYCHQYSKLPWTFCQGTKEIKR 108  
Db |||||  
81 RFSGGSGGTDYTLTITSSLPQDFATYCHQYSKLPWTFCQGTKEIKR 128

RESULT 7  
AAB81992  
ID AAB81992 standard; protein; 128 AA.  
XX  
AC AAB81992;  
XX  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD3 specific antibody related protein #3.  
XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
XX  
OS Synthetic.  
XX  
PN WO200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
XX  
PR 30-SEP-1999; 99JP-00278291.  
XX  
PR 06-APR-2000; 2000JP-00105088.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
DR WPI; 2001-266143/27.  
XX  
DR N-PSDB; AAF86898.  
XX  
New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX  
PS Example 1; Page 155-156; 183pp; Japanese.  
XX  
The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumours, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX  
SQ Sequence 128 AA;

Query Match 97.2%; Score 558; DB 4; Length 128;  
Best Local Similarity 98.1%; Pred. No. 2.2e-33;  
Matches 106; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60  
Db |||||  
QY 21 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 80  
61 RFSGGSGGTDYTLTITSSLPQDFATYCHQYSKLPWTFCQGTKEIKR 108  
Db |||||  
81 RFSGGSGGTDYTLTITSSLPQDFATYCHQYSKLPWTFCQGTKEIKR 128

XX 03-JUL-2001 (first entry)  
DT Ganglioside GD3 specific antibody related protein #1.  
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;  
DE cancer.  
KW Synthetic.  
KW WO200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
XX  
PR 30-SEP-1999; 99JP-00278291.  
XX  
PR 06-APR-2000; 2000JP-00105088.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
DR WPI; 2001-266143/27.  
XX  
DR N-PSDB; AAF86892.  
XX  
New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX  
PS Example 1; Page 150-151; 183pp; Japanese.  
XX  
The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumours, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX  
SQ Sequence 128 AA;

Query Match 97.2%; Score 558; DB 4; Length 128;  
Best Local Similarity 97.2%; Pred. No. 2.2e-33;  
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60  
Db |||||  
QY 21 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 80  
61 RFSGGSGGTDYTLTITSSLPQDFATYCHQYSKLPWTFCQGTKEIKR 108  
Db |||||  
81 RFSGGSGGTDYTLTITSSLPQDFATYCHQYSKLPWTFCQGTKEIKR 128

RESULT 8  
AAB11011  
ID AAB11011 standard; protein; 108 AA.  
XX  
AC AAB11011;  
XX  
DT 04-FEB-2003 (first entry)  
XX  
DE Modified ganglioside GD3 antibody associated protein #4.  
XX  
KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.  
XX  
OS Synthetic.  
XX  
PN WO200278739-A1.  
XX  
PD 10-OCT-2002.  
XX  
PF 29-MAR-2002; 2002WO-JP003170.

XX 29-MAR-2001; 2001JP-00097483.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX Shitara K, Niwa R, Kanazawa J, Asada M;  
XX WPI; 2003-067410/06.  
XX  
XX Drugs containing genetically-modified antibody against ganglioside GD3,  
PT its fragment, immunocompetent cell activators or/and antitumor agents in  
PT combination, applicable in treating malignant tumor like melanoma.  
XX  
XX Claim 8; Page 100; 121pp; Japanese.  
XX  
XX The invention describes drugs contain a genetically-modified antibody  
CC against ganglioside GD3 or its fragment and at least 1 of a substance  
CC capable of activating immunocompetent cells and a substance having an  
CC antitumor activity in combination. The drugs can be used to treat tumor  
CC like melanoma and can provide a treatment with enhanced therapeutic  
CC effect and little side-reactions, particularly to relieve problems of  
CC side-effects during the conventional single administration. This sequence  
CC represents a protein associated with the anti- ganglioside GD3 antibody  
XX  
XX Sequence 108 AA;  
SQ

Query Match 97.0%; Score 557; DB 6; Length 108;  
Best Local Similarity 97.2%; Pred. No. 2.3e-33;  
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNWYQOKPGKAPKLLIFYSSNLHSGVPS 60  
DB 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNWYQOKPGKAPKLLIFYSSNLHSGVPS 60  
QY 61 RFSGGSGTDYTLTISSLPEDATYFCHQYSKLPWTFGGQTKVEIKR 108  
DB 61 RFSGGSGTDYTLTISSLPEDATYFCHQYSKLPWTFGGQTKVEIKR 108

RESULT 9  
AAB81988  
ID AAB81988 standard; protein; 108 AA.  
AC AAB81988;  
XX  
XX 03-JUL-2001 (first entry)  
XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 54.  
DE Ganglioside; GD3; complementarity determining region; CDR; antibody;  
XX cancer.  
XX Synthetic.  
XX WO200123432-A1.  
XX  
XX 05-APR-2001.  
XX  
XX 29-SEP-2000; 2000WO-JP006774.  
XX  
XX 30-SEP-1999; 99JP-00278291.  
XX 06-APR-2000; 2000JP-00105088.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX Hanai N, Shitara K, Nakamura K, Niwa R;  
XX WPI; 2001-266143/27.  
XX  
XX New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.

Query Match 95.5%; Score 548; DB 4; Length 128;  
Best Local Similarity 96.3%; Pred. No. 1.2e-32;  
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNWYQOKPGKAPKLLIFYSSNLHSGVPS 60  
DB 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNWYQOKPGKAPKLLIFYSSNLHSGVPS 60  
QY 61 RFSGGSGTDYTLTISSLPEDATYFCHQYSKLPWTFGGQTKVEIKR 108  
DB 61 RFSGGSGTDYTLTISSLPEDATYFCHQYSKLPWTFGGQTKVEIKR 108

RESULT 10  
AAB81999  
ID AAB81999 standard; protein; 128 AA.  
AC AAB81999;  
XX  
XX 03-JUL-2001 (first entry)  
XX Ganglioside GD3 specific antibody related protein #8.  
DE Ganglioside; GD3; complementarity determining region; CDR; antibody;  
XX cancer.  
XX Synthetic.  
XX WO200123432-A1.  
XX  
XX 05-APR-2001.  
XX  
XX 29-SEP-2000; 2000WO-JP006774.  
XX  
XX 30-SEP-1999; 99JP-00278291.  
XX 06-APR-2000; 2000JP-00105088.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX Hanai N, Shitara K, Nakamura K, Niwa R;  
XX WPI; 2001-266143/27.  
XX  
XX New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.

Query Match 95.5%; Score 548; DB 4; Length 128;  
Best Local Similarity 96.3%; Pred. No. 1.2e-32;  
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNWYQOKPGKAPKLLIFYSSNLHSGVPS 60  
DB 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNWYQOKPGKAPKLLIFYSSNLHSGVPS 60  
QY 61 RFSGGSGTDYTLTISSLPEDATYFCHQYSKLPWTFGGQTKVEIKR 108  
DB 61 RFSGGSGTDYTLTISSLPEDATYFCHQYSKLPWTFGGQTKVEIKR 108

RESULT 10  
AAB81999  
ID AAB81999 standard; protein; 128 AA.  
AC AAB81999;  
XX  
XX 03-JUL-2001 (first entry)  
XX Ganglioside GD3 specific antibody related protein #8.  
DE Ganglioside; GD3; complementarity determining region; CDR; antibody;  
XX cancer.  
XX Synthetic.  
XX WO200123432-A1.  
XX  
XX 05-APR-2001.  
XX  
XX 29-SEP-2000; 2000WO-JP006774.  
XX  
XX 30-SEP-1999; 99JP-00278291.  
XX 06-APR-2000; 2000JP-00105088.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX Hanai N, Shitara K, Nakamura K, Niwa R;  
XX WPI; 2001-266143/27.  
XX  
XX New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.

```
QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNWTQKPGKAPKLLIFYSNHLHSGVPS 60
DB 21 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNWTQKPGKAPKLLIFYSNHLHSGVPS 80
QY 61 RFSGGSGGTDYTLTSSSLQPEDFATYCHQYKSLPWTFCQGTKEIKR 108
DB 81 RFSGGSGGTDYTLTSSSLQPEDFATYCHQYKSLPWTFCQGTKEIKR 128

RESULT 11
AAB81998
ID AAB81998 standard; protein; 128 AA.
XX
AC AAB81998;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #7.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
DR N-PSDB; AAF86912.
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 3; Page 164-165; 183pp; Japanese.
XX
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;
Query Match 95.5%; Score 548; DB 4; Length 128;
Best Local Similarity 96.3%; Pred. No. 1.2e-32;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNWTQKPGKAPKLLIFYSNHLHSGVPS 60
DB 21 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNWTQKPGKAPKLLIFYSNHLHSGVPS 80
QY 61 RFSGGSGGTDYTLTSSSLQPEDFATYCHQYKSLPWTFCQGTKEIKR 108
DB 81 RFSGGSGGTDYTLTSSSLQPEDFATYCHQYKSLPWTFCQGTKEIKR 128

RESULT 12
AAW70673
ID AAW70673 standard; peptide; 110 AA.
XX
```

```
AC AAW70673;
XX 27-JAN-1999 (first entry)
XX
DE Anti-VEGF humanised antibody variable light domain of template MB1.6.
XX
KW Light variable domain; murine; humanised antibody;
KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
KW VEGF-induced angiogenesis; tumour; retinal disorder;
KW age-related macular degeneration; diabetic retinopathy;
KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
PN WO9845331-A2.
XX
PD 15-OCT-1998.
XX
PF 03-APR-1998; 98WO-US006604.
XX
PR 07-APR-1997; 97US-00833504.
PR 06-AUG-1997; 97US-00908469.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX
DR WPI; 1998-568337/48.
XX
PT New humanised antibody with affinity for vascular endothelial growth
PT factor - for treatment of tumours, retinal disease and other angiogenic
PT states, also related nucleic acid, vectors and transformed cells.
XX
PS Example 3; Fig 9A; 100pp; English.
XX
CC The present sequence represents a variable light domain of the template
CC molecule of the affinity-matured anti-vascular endothelial growth factor
CC (anti-VEGF) antibody. The sequence is used in the course of the invention
CC to produce the humanised anti-VEGF antibody of the invention. The
CC humanised antibodies are used to inhibit VEGF-induced angiogenesis,
CC particularly for treating or preventing tumours (of any type) and retinal
CC disorders (e.g. age-related macular degeneration or diabetic
CC retinopathy). They can also be used to treat other conditions that
CC involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,
CC atherosclerosis, Grave's disease, etc
XX
SQ Sequence 110 AA;
Query Match 92.9%; Score 533; DB 2; Length 110;
Best Local Similarity 91.7%; Pred. No. 1.3e-31;
Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNWTQKPGKAPKLLIFYSNHLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNWTQKPGKAPKLLIFYSNHLHSGVPS 60
QY 61 RFSGGSGGTDYTLTSSSLQPEDFATYCHQYKSLPWTFCQGTKEIKR 108
DB 61 RFSGGSGGTDYTLTSSSLQPEDFATYCHQYKSLPWTFCQGTKEIKR 108

RESULT 13
ABP61242
ID ABP61242 standard; protein; 110 AA.
XX
AC ABP61242;
XX
DT 20-SEP-2002 (first entry)
XX
DE Humanised anti-VEGF MB1.6 antibody variable light domain.
XX
```

KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;  
 KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;  
 KW retinal disorder; intraocular neovascular disorder; MB1.6; light chain;  
 KW variable domain.

XX Homo sapiens.  
 OS Mus sp.  
 OS Synthetic.

XX Key Location/Qualifiers  
 XX Domain 24..34  
 FT /label= CDR-L1  
 FT Domain 50..57  
 FT /label= CDR-L2  
 FT Domain 89..97  
 FT /label= CDR-L3

XX US2002032315-A1.

XX 14-MAR-2002.

XX 06-APR-1998; 98US-00056160.

XX 06-AUG-1997; 97US-0054856P.

XX (BACA/) BACA M.  
 XX (WELL/) WELLS J A.  
 XX (PRES/) PRESTA L G.  
 XX (LOWM/) LOWMAN H B.  
 XX (CHEN/) CHEN Y M.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI; 2002-517920/55.

XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies  
 FT or their variants, useful for inhibiting VEGF-induced angiogenesis in a  
 FT mammal, particularly for treating tumor or retinal disorders.

XX Example 3; Fig 9; 47pp; English.

XX The present invention relates to humanised anti-VEGF (vascular  
 CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF  
 CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for  
 CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human).  
 CC particularly those having a tumour or a retinal disorder e.g. intraocular  
 CC neovascular disorders. The present sequence is an exemplary light chain  
 CC variable domain of the humanised anti-VEGF antibody of the invention

XX Sequence 110 AA;

Query Match 92.9%; Score 533; DB 5; Length 110;  
 Best Local Similarity 91.7%; Pred. No. 1.3e-31;  
 Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNHLGVPVS 60  
 Db 1 DIQLTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNHLGVPVS 60

QY 61 RFSGSGSGTDYTLTISSLPEDPATYVCHQYKLPWTFGGTKVEIKR 108  
 Db 61 RFSGSGSGTDYTLTISSLPEDPATYVCHQYKLPWTFGGTKVEIKR 108

RESULT 14

AAW70703

ID AAW70703 standard; protein; 237 AA.

XX AAW70703;

XX 27-JAN-1999 (first entry)

DE Protein encoded by Fab-display antibody vector phMB4-19-1.6.

XX Murine; humanised antibody; VEGF-induced angiogenesis; tumour;  
 KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;  
 KW retinal disorder; age-related macular degeneration; diabetic retinopathy;  
 KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

XX Synthetic.

XX WO9845331-A2.

XX 15-OCT-1998.

XX 03-APR-1998; 98WO-US006604.

XX 07-APR-1997; 97US-00833504.

XX 06-AUG-1997; 97US-00908469.

XX (GETH ) GENENTECH INC.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI; 1998-568337/48.

XX N-PSDB; AAV63493.

XX New humanised antibody with affinity for vascular endothelial growth  
 FT factor - for treatment of tumours, retinal disease and other angiogenic  
 FT states, also related nucleic acid, vectors and transformed cells.

XX Example 3; Fig 8A-E; 100pp; English.

XX The present sequence is encoded by the Fab-display antibody vector phMB4-  
 CC 19-1.6, which is used in the course of the invention. The specification  
 CC describes humanised murine anti-vascular endothelial growth factor (anti-  
 CC VEGF) antibodies. The humanised antibodies are used to inhibit VEGF-  
 CC induced angiogenesis, particularly for treating or preventing tumours (of  
 CC any type) and retinal disorders (e.g. age-related macular degeneration  
 CC or diabetic retinopathy). They can also be used to treat other conditions  
 CC that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,  
 CC atherosclerosis, Grave's disease, etc

XX Sequence 237 AA;

Query Match 92.9%; Score 533; DB 2; Length 237;  
 Best Local Similarity 91.7%; Pred. No. 2.6e-31;  
 Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNHLGVPVS 60  
 Db 24 DIQLTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNHLGVPVS 83

QY 61 RFSGSGSGTDYTLTISSLPEDPATYVCHQYKLPWTFGGTKVEIKR 108

Db 84 RFSGSGSGTDYTLTISSLPEDPATYVCHQYKLPWTFGGTKVEIKR 131

RESULT 15

ABP61241

ID ABP61241 standard; protein; 650 AA.

XX ABP61241;

XX 20-SEP-2002 (first entry)

DE Phage-display antibody vector phMB4-19-1.6 protein.

XX Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;

KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;  
 KW retinal disorder; intraocular neovascular disorder; phMB4-19-1.6.

XX Synthetic.

XX Key

Location/Qualifiers

FT Peptide 1..23

```
FT Protein /label= Signal_peptide
FT 24..237
FT /label= Light_chain_region
FT Peptide 238..260
FT /label= Signal_peptide
FT Protein 261..491
FT /label= Heavy_chain_region
FT /note= "Fused to g3p domain"
FT Misc-difference 492
FT /note= "Encoded by stop codon"
FT 493
FT Protein /label= Truncated g3p_domain.protein
FT /note= "Fused to heavy_chain"
FT
XX
PN US2002032315-A1.
XX
XX 14-MAR-2002.
XX
XX 06-APR-1998; 98US-00056160.
XX
XX 06-AUG-1997; 97US-0054856P.
XX
XX (BACA/) BACA M.
XX (WELL/) WELLS J A.
XX (PRES/) PRESTA L G.
XX (LOWN/) LOWMAN H B.
XX (CHEN/) CHEN Y M.
XX
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX WPI: 2002-517920/55.
XX N-PSDB; ABN85200.
XX
XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies
XX or their variants, useful for inhibiting VEGF-induced angiogenesis in a
XX mammal, particularly for treating tumor or retinal disorders.
XX
XX Example 3; Fig 8; 47pp; English.
XX
XX The present invention relates to humanised anti-VEGF (vascular
XX endothelial growth factor) antibodies or a variant of a parent anti-VEGF
XX antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
XX inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
XX particularly those having a tumour or a retinal disorder e.g. intraocular
XX neovascular disorders. The present sequence is the protein encoded by
XX phage-display antibody vector pMB4-19-1.6. This sequence was used as a
XX parent during the construction of humanised antibody pY101. In the pMB4
XX -19-1.6 construct, anti-VEGF is expressed as a Fab fragment with its
XX heavy chain fused to the N-terminus of the truncated g3p. Both the light
XX and heavy chains are under the control of phoA promoter with an upstream
XX still signal-sequence for secretion into the periplasm
XX
XX Sequence 650 AA;
SQ
Query Match 92.9%; Score 533; DB 5; Length 650;
Best Local Similarity 91.7%; Pred. No. 6.4e-31; Indels 0; Gaps 0;
Matches 99; Conservative 6; Mismatches 3;
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
DB 24 DIQLTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIYFTSSLHSGVPS 83
QY 61 RFSGGSGGTDYTLTITSSLPEDPATYCHQYKLPWTFCGGTKVEIKR 108
DB 84 RFSGGSGGTDYTLTITSSLPEDPATYCHQYKLPWTFCGGTKVEIKR 131
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Search completed: August 1, 2005, 09:10:03  
Job time : 35.5277 secs

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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:59:16 ; Search time 8.1913 Seconds  
(without alignments)  
983.287 Million cell updates/sec

Title: US-10-089-500-10

Perfect score: 574

Sequence: 1 DIQMTQSPSLASVGRVT.....HOVSKLPWTFGQTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA.\*

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6: /cgn2\_6/ptodata/1/iaa/backfilesi.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	529	92.2	110	4	US-09-440-781-94
3	507	88.3	110	4	US-09-440-781-95
4	506	88.2	107	2	US-07-934-373C-17
5	506	88.2	107	3	US-08-437-642B-17
6	506	88.2	107	4	US-08-146-206C-17
7	506	88.2	107	4	US-09-705-686-17
8	506	88.2	107	4	US-09-705-392A-17
9	506	88.2	107	5	PCT-US93-07832-17
10	506	88.2	109	2	US-07-934-373C-47
11	506	88.2	109	3	US-08-437-642B-47
12	506	88.2	109	3	US-08-437-642B-47
13	506	88.2	127	3	US-08-649-100-33
14	506	88.2	214	2	US-07-934-373C-40
15	506	88.2	214	2	US-08-788-800-11
16	506	88.2	214	3	US-08-437-642B-40
17	506	88.2	214	3	US-09-097-309-2
18	506	88.2	214	3	US-09-097-171A-2
19	506	88.2	214	3	US-09-460-587-2
20	506	88.2	214	4	US-09-940-166A-2
21	506	88.2	214	5	PCT-US93-07832-40
22	506	88.2	233	2	US-07-934-373C-25
23	506	88.2	233	3	US-08-437-642B-25
24	506	88.2	233	4	US-08-146-206C-25
25	506	88.2	233	4	US-09-705-686-25
26	506	88.2	233	4	US-09-705-392A-25
27	506	88.2	233	4	US-09-705-398-25

28	506	88.2	233	5	PCT-US93-07832-25	Sequence 25, Appl
29	506	88.2	237	3	US-09-097-309-6	Sequence 6, Appl
30	506	88.2	237	3	US-09-097-171A-10	Sequence 10, Appl
31	506	88.2	237	3	US-09-422-712B-2	Sequence 2, Appl
32	506	88.2	237	3	US-09-607-756-2	Sequence 2, Appl
33	506	88.2	237	3	US-09-460-587-6	Sequence 6, Appl
34	506	88.2	237	4	US-09-940-166A-6	Sequence 6, Appl
35	503	87.6	214	1	US-08-458-516-12	Sequence 12, Appl
36	501	87.3	108	3	US-08-974-899-3	Sequence 3, Appl
37	501	87.3	108	4	US-09-795-798-3	Sequence 3, Appl
38	498	86.8	107	1	US-08-458-516-8	Sequence 8, Appl
39	498	86.8	107	2	US-07-934-373C-39	Sequence 39, Appl
40	498	86.8	214	3	US-08-437-642B-39	Sequence 39, Appl
41	498	86.8	214	5	PCT-US93-07832-39	Sequence 39, Appl
42	496	86.4	107	2	US-07-934-373C-18	Sequence 18, Appl
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45	496	86.4	107	4	US-08-146-206C-18	Sequence 18, Appl
46	496	86.4	107	4	US-09-648-067A-14	Sequence 14, Appl
47	496	86.4	107	4	US-09-705-686-18	Sequence 18, Appl
48	496	86.4	107	4	US-09-705-392A-18	Sequence 18, Appl
49	496	86.4	107	4	US-09-705-398-18	Sequence 18, Appl
50	496	86.4	107	5	PCT-US93-07832-18	Sequence 18, Appl
51	494	86.1	128	4	US-09-225-322B-10	Sequence 10, Appl
52	494	86.1	128	4	US-09-225-322B-19	Sequence 19, Appl
53	494	86.1	128	4	US-09-764-304-10	Sequence 10, Appl
54	494	86.1	128	4	US-09-764-304-19	Sequence 19, Appl
55	492	85.7	107	3	US-09-254-189-1	Sequence 1, Appl
56	492	85.7	109	2	US-07-934-373C-3	Sequence 3, Appl
57	492	85.7	109	3	US-08-437-642B-3	Sequence 3, Appl
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59	492	85.7	109	4	US-09-705-686-3	Sequence 3, Appl
60	492	85.7	109	4	US-09-705-392A-3	Sequence 3, Appl
61	492	85.7	109	4	US-09-705-398-3	Sequence 3, Appl
62	492	85.7	109	5	PCT-US93-07832-3	Sequence 3, Appl
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64	491	85.5	111	1	US-08-137-117D-67	Sequence 67, Appl
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67	491	85.5	126	2	US-08-436-717-71	Sequence 71, Appl
68	491	85.5	212	4	US-10-011-125A-5	Sequence 5, Appl
69	489	85.2	109	4	US-09-802-083-4	Sequence 4, Appl
70	488	85.0	109	3	US-09-157-370-3	Sequence 3, Appl
71	486.5	84.8	114	2	US-08-561-521-43	Sequence 43, Appl
72	486.5	84.8	114	5	PCT-US95-01219-43	Sequence 43, Appl
73	482	84.0	102	3	US-09-199-149-10	Sequence 10, Appl
74	482	84.0	108	3	US-09-199-149-14	Sequence 14, Appl
75	481	83.8	108	3	US-09-025-768B-14	Sequence 14, Appl
76	481	83.8	108	4	US-09-490-070A-14	Sequence 14, Appl
77	481	83.8	108	4	US-09-490-153-14	Sequence 14, Appl
78	481	83.8	108	4	US-09-490-324-14	Sequence 14, Appl
79	478	83.3	107	2	US-08-318-157B-6	Sequence 6, Appl
80	478	83.3	107	2	US-09-253-79A-6	Sequence 6, Appl
81	478	83.3	127	3	US-08-836-561-71	Sequence 71, Appl
82	478	83.3	127	4	US-09-434-122-71	Sequence 71, Appl
83	477	83.1	234	4	US-09-740-002-24	Sequence 24, Appl
84	474	82.6	111	2	US-08-887-352B-7	Sequence 7, Appl
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87	474	82.6	111	4	US-09-920-171-7	Sequence 7, Appl
88	474	82.6	111	4	US-09-716-028-7	Sequence 7, Appl
89	474	82.6	111	4	US-10-113-996-7	Sequence 7, Appl
90	474	82.6	127	4	US-09-809-739-10	Sequence 10, Appl
91	474	82.6	218	5	PCT-US96-13152-2	Sequence 2, Appl
92	474	82.6	263	3	US-09-069-821-3	Sequence 3, Appl
93	474	82.6	263	4	US-09-956-086-3	Sequence 3, Appl
94	474	82.6	263	4	US-09-956-087-3	Sequence 3, Appl
95	474	82.6	283	3	US-09-420-592A-6	Sequence 6, Appl
96	474	82.6	283	4	US-09-985-442-6	Sequence 6, Appl
97	474	82.6	283	4	US-09-983-580-6	Sequence 6, Appl
98	472.5	82.3	114	1	US-08-202-047-25	Sequence 25, Appl
99	472.5	82.3	114	3	US-08-964-690-25	Sequence 25, Appl
100	472.5	82.3	116	1	US-08-478-039-83	Sequence 83, Appl

## ALIGNMENTS

```

RESULT 1
US-10-011-125A-2
; Sequence 2, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: PI804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
US-10-011-125A-2

Query Match          92.9%; Score 533; DB 4; Length 491;
Best Local Similarity 91.7%; Pred. No. 4.8e-43;
Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy      1  DIQWTQSPSSLSASVGRVVTITCSASODISNYLNNWYQOKPKAPKLLIFYSNNLHSGVPS 60
Db      24  DIQUTQSPSSLSASVGRVVTITCSASQDISNYLNNWYQOKPKAPKLLIYFTSSLHSGVPS 83

Qy      61  RFSGGSGGTDYTLTITSSLPQEDFATYYCHQYSKLPWTFGGQTKVEIKR 108
Db      84  RFSGGSGGTDYTLTITSSLPQEDFATYYCQYSTVPWTFGGQTKVEIKR 131

RESULT 2
US-09-440-781-94
; Sequence 94, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-vee Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: PI469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 94
; LENGTH: 110
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-110
; OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-94

Query Match          92.2%; Score 529; DB 4; Length 110;
Best Local Similarity 90.7%; Pred. No. 2.2e-43;
Matches 99; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy      1  DIQWTQSPSSLSASVGRVVTITCSASODISNYLNNWYQOKPKAPKLLIFYSNNLHSGVPS 60
Db      1  DIQWTQSPSSLSASVGRVVTITCSASQDISNYLNNWYQOKPKAPKLLIYFTSSLHSGVPS 60

Qy      61  RFSGGSGGTDYTLTITSSLPQEDFATYYCHQYSKLPWTFGGQTKVEIKR 108
Db      61  RFSGGSGGTDYTLTITSSLPQEDFATYYCQYSTVPWTFGGQTKVEIKR 108

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; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-17

Query Match      88.2%; Score 506; DB 2; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.3e-41;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDINSYLNWYQKPGKAPKLLIFYSNNLHSGVPS 60
   |||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDIRNLYNWYQKPGKAPKLLIYTSRLESGVPS 60
   |||||

QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYSKLPMTFGGQTKVEIK 107
   |||||
Db 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYSKLPMTFGGQTKVEIK 107
   |||||

RESULT 5
US-08-437-642B-17
; Sequence 17, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-17

Query Match      88.2%; Score 506; DB 3; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.3e-41;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDINSYLNWYQKPGKAPKLLIFYSNNLHSGVPS 60
   |||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDIRNLYNWYQKPGKAPKLLIYTSRLESGVPS 60
   |||||

QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYSKLPMTFGGQTKVEIK 107
   |||||
Db 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYSKLPMTFGGQTKVEIK 107
   |||||

RESULT 6
US-08-146-206C-17
; Sequence 17, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-146-206C-17

Query Match      88.2%; Score 506; DB 4; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.3e-41;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDINSYLNWYQKPGKAPKLLIFYSNNLHSGVPS 60
   |||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDIRNLYNWYQKPGKAPKLLIYTSRLESGVPS 60
   |||||

QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYSKLPMTFGGQTKVEIK 107
   |||||
Db 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYSKLPMTFGGQTKVEIK 107
   |||||

RESULT 7
US-09-705-686-17
; Sequence 17, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.

```

;; TITLE OF INVENTION: Method for Making Humanized Antibodies  
;; NUMBER OF SEQUENCES: 26  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Genentech, Inc.  
;; STREET: 1 DNA Way  
;; CITY: South San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94080  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WinPatIn (Genentech)  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/705,686  
;; FILING DATE: 02-No. 6639055-2000  
;; CLASSIFICATION: <Unknown>  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/146206  
;; FILING DATE: 17-NOV-1993  
;; APPLICATION NUMBER: 07/715272  
;; FILING DATE: 14-JUN-1991  
;;  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Lee, Wendy M.  
;; REGISTRATION NUMBER: 40,378  
;; REFERENCE/DOCKET NUMBER: P0709PID3  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650/225-1994  
;; TELEFAX: 650/952-9881  
;;  
;; INFORMATION FOR SEQ ID NO: 17:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 107 amino acids  
;; TYPE: Amino Acid  
;; TOPOLOGY: Linear  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-705-686-17  
Query Match 88.2%; Score 506; DB 4; Length 107;  
Best Local Similarity 89.7%; Pred. No. 3.3e-41;  
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60  
Db 1 DIQMTQSPSSLSASVGDRVTITCSASQDIRNLYNWYQKPGKAPKLLIYTSRLSGVPS 60  
QY 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYKLPWTFQGGTKVEIK 107  
Db 61 RFGSGSGTDYTLTISSLPEDFATYYCQGGNTLPWTFQGGTKVEIK 107  
RESULT 8  
US-09-705-392A-17  
; Sequence 17, Application US/09705392A  
; Patent No. 6719971  
; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; Presta, Leonard G.  
; TITLE OF INVENTION: Method for Making Humanized Antibodies  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/705,392A  
;; FILING DATE: 02-No. 6719971-2002  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/146206  
;; FILING DATE: 17-NOV-1993  
;; APPLICATION NUMBER: 07/715272  
;; FILING DATE: 14-JUN-1991  
;;  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Lee, Wendy M.  
;; REGISTRATION NUMBER: 40,378  
;; REFERENCE/DOCKET NUMBER: P0709PID1 REVISED  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650/225-1994  
;; TELEFAX: 650/952-9881  
;;  
;; INFORMATION FOR SEQ ID NO: 17:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 107 amino acids  
;; TYPE: Amino Acid  
;; TOPOLOGY: Linear  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-705-392A-17  
Query Match 88.2%; Score 506; DB 4; Length 107;  
Best Local Similarity 89.7%; Pred. No. 3.3e-41;  
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60  
Db 1 DIQMTQSPSSLSASVGDRVTITCSASQDIRNLYNWYQKPGKAPKLLIYTSRLSGVPS 60  
QY 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYKLPWTFQGGTKVEIK 107  
Db 61 RFGSGSGTDYTLTISSLPEDFATYYCQGGNTLPWTFQGGTKVEIK 107  
RESULT 9  
US-09-705-398-17  
; Sequence 17, Application US/09705398  
; Patent No. 6800738  
; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; Presta, Leonard G.  
; TITLE OF INVENTION: Method for Making Humanized Antibodies  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/705,398  
; FILING DATE: 02-No. 6800738-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/146206  
; FILING DATE: 17-NOV-1993  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709PID2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881

```

; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-705-398-17

Query Match      88.2%; Score 506; DB 4; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.3e-41;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDINYNLWYQKPGKAPKLLIFYSNHLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDIRNLYNWYQKPGKAPKLLIYTSRLESGVPS 60
Qy 61 RFSGSGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIK 107
Db 61 RFSGSGSGTDYTLTISSLPEDFATYYCQGNLPLPWTFGQGTKEIK 107

RESULT 10
PCT-US93-07832-17
; Sequence 17, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 15-JUN-1992
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELEPHONE: 415/952-9881
; TELEFAX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US93-07832-17

Query Match      88.2%; Score 506; DB 5; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.3e-41;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDINYNLWYQKPGKAPKLLIFYSNHLHSGVPS 60

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Db 1 DIQMTQSPSSLSASVGRVTITCRASQDIRNLYNWYQKPGKAPKLLIYTSRLESGVPS 60
Qy 61 RFSGSGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIK 107
Db 61 RFSGSGSGTDYTLTISSLPEDFATYYCQGNLPLPWTFGQGTKEIK 107

RESULT 11
US-07-934-373C-47
; Sequence 47, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-47

Query Match      88.2%; Score 506; DB 2; Length 109;
Best Local Similarity 89.8%; Pred. No. 3.4e-41;
Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDINYNLWYQKPGKAPKLLIFYSNHLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDIRNLYNWYQKPGKAPKLLIYTSRLESGVPS 60
Qy 61 RFSGSGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIKR 108
Db 61 RFSGSGSGTDYTLTISSLPEDFATYYCQGNLPLPWTFGQGTKEIKR 108

RESULT 12
US-08-437-642B-47
; Sequence 47, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta

```

```

; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: 07/715272
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-08-437-642B-47
;
; Query Match 88.2%; Score 506; DB 3; Length 109;
; Best Local Similarity 89.8%; Pred. No. 3.4e-41;
; Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
;
; QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
; DB 1 DIQMTQSPSSLSASVGDRTVITCRASQDISNNYLNWYQKPGKAPKLLIYTTLSHGVP 60
;
; QY 61 RFSGGSGTDYTLTISLQPEDFATYCHQYKLPWTFGGTKVEIKR 108
; DB 61 RFSGGSGTDYTLTISLQPEDFATYCHQYKLPWTFGGTKVEIKR 108
;
; RESULT 13
; US-08-649-100-33
; Sequence 33, Application US/08649100
; Patent No. 6114507
; GENERAL INFORMATION:
; APPLICANT: SHIRAKAWA, KAMON
; APPLICANT: MATSUE, TOMOKAZU
; APPLICANT: NAGATA, SHIGEKAZU
; APPLICANT: CO. MAN SHING
; APPLICANT: VASQUEZ, MAXIMILIANO
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
; METHOD OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
;
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,100
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-649-100-33
;
; Query Match 88.2%; Score 506; DB 3; Length 127;
; Best Local Similarity 87.9%; Pred. No. 4e-41;
; Matches 94; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
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; QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
; DB 21 DIQMTQSPSTLSASVGDRTVITCRASQDISNYLNWYQKPGKAPKLLIYTTLSHGVP 80
;
; QY 61 RFSGGSGTDYTLTISLQPEDFATYCHQYKLPWTFGGTKVEIK 107
; DB 81 RFSGGSGTNYTLTISLQPDFFATYFCQGSSTLPWTFGGTKVEIK 127
;
; RESULT 14
; US-07-934-373C-40
; Sequence 40, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991

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; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-07-934-373C-40

Query Match 88.2%; Score 506; DB 2; Length 214;
Best Local Similarity 89.8%; Pred. No. 7.2e-41;
Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCSASQDISNLYLNWYQOKFGKAPKLLIFYSSNLHSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQDINNLYLNWYQOKFGKAPKLLIYYTSTLHSGVPS 60
Qy 61 RFSGSGSGTDYTLTISSLOPEDFATYYCHQYSKLPWTFGGGTVKVEIKR 108
Db 61 RFSGSGSGTDYTLTISSLOPEDFATYYCQGGNTLPPTFGGGTVKVEIKR 108

RESULT 15
US-08-788-800-11
; Sequence 11, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELE: 910/371-7168
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-788-800-11

Query Match 88.2%; Score 506; DB 2; Length 214;
Best Local Similarity 89.8%; Pred. No. 7.2e-41;
Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCSASQDISNLYLNWYQOKFGKAPKLLIFYSSNLHSGVPS 60
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Db 1 DIQWTQSPSSLSASVGDRTVITCRASQDINNLYLNWYQOKFGKAPKLLIYYTSTLHSGVPS 60
Qy 61 RFSGSGSGTDYTLTISSLOPEDFATYYCHQYSKLPWTFGGGTVKVEIKR 108
Db 61 RFSGSGSGTDYTLTISSLOPEDFATYYCQGGNTLPPTFGGGTVKVEIKR 108

Search completed: August 1, 2005, 09:20:50
Job time : 10.1991 secs
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85 507 88.3 110 17 US-10-974-591-111  
86 507 88.3 110 17 US-10-974-591-113  
87 506 88.2 107 16 US-10-835-641-17  
88 506 88.2 127 14 US-10-084-139-6  
89 506 88.2 214 9 US-09-940-166A-2  
90 506 88.2 214 9 US-09-811-384-11  
91 506 88.2 214 15 US-10-404-286-11  
92 506 88.2 214 16 US-10-762-967-2  
93 506 88.2 214 20 US-11-077-717-2  
94 506 88.2 233 16 US-10-835-641-25  
95 506 88.2 237 9 US-09-940-166A-6  
96 506 88.2 237 14 US-10-227-694-1  
97 506 88.2 237 16 US-10-762-967-6  
98 506 88.2 237 17 US-10-754-212-2  
99 506 88.2 237 20 US-11-077-717-10  
100 503 87.6 103 16 US-10-379-392-100

## ALIGNMENTS

## RESULT 1

US-09-056-160B-103  
; Sequence 103, Application US/09056160B

; Patent No. US20020032315A1

; GENERAL INFORMATION:

; APPLICANT: Baca, Manuel

; APPLICANT: Wells, James A.

; APPLICANT: Presta, Leonard G.

; APPLICANT: Lowman, Henry B.

; APPLICANT: Chen, Yvonne M.

; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

; NUMBER OF SEQUENCES: 131

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/056,160B

; FILING DATE: 06-Apr-1998

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/054,856

; FILING DATE: 06-AUG-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hasak, Janet E.

; REGISTRATION NUMBER: 28,616

; REFERENCE/DOCKET NUMBER: P1093R2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1896

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 103:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 110 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-09-056-160B-103

Query Match

Best Local Similarity 92.9%; Score 533; DB 9; Length 110;

Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLSHGVPs 60

Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLSHGVPs 60

Sequence 111, App  
Sequence 113, App  
Sequence 17, Appl  
Sequence 6, Appl  
Sequence 2, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 25, Appl  
Sequence 6, Appl  
Sequence 1, Appl  
Sequence 6, Appl  
Sequence 2, Appl  
Sequence 10, Appl  
Sequence 100, App

QY

61 RPSGGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIKR 108

Db

61 RPSGGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIKR 108

## RESULT 2

US-10-234-671-101

; Sequence 101, Application US/10234671

; Publication No. US20030190317A1

; GENERAL INFORMATION:

; APPLICANT: Baca, Manuel

; APPLICANT: Wells, James A.

; APPLICANT: Presta, Leonard G.

; APPLICANT: Lowman, Henry B.

; APPLICANT: Chen, Yvonne M.

; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

; NUMBER OF SEQUENCES: 131

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/234,671

; FILING DATE: 03-Sep-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/056160

; FILING DATE: 06-APR-1998

; APPLICATION NUMBER: 60/126446

; FILING DATE: 07-APR-1997

; APPLICATION NUMBER: 60/054856

; FILING DATE: 06-AUG-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Cui, Steven X.

; REGISTRATION NUMBER: 44,637

; REFERENCE/DOCKET NUMBER: P1093R2C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-8674

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 101:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 110 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 101:

US-10-234-671-101

Query Match

Best Local Similarity 92.9%; Score 533; DB 14; Length 110;

Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLSHGVPs 60

Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLSHGVPs 60

QY 61 RPSGGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIKR 108

Db 61 RPSGGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIKR 108

## RESULT 3

US-10-974-591-101

; Sequence 101, Application US/10974591

; Publication No. US20050112126A1







CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/056.160B  
 FILING DATE: 06-Apr-1998  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/054,856  
 FILING DATE: 06-AUG-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hasek, Janet E.  
 REGISTRATION NUMBER: 28,616  
 REFERENCE/DOCKET NUMBER: P1093R2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-1896  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 107 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 US-09-056-160B-15

Query Match 92.5%; Score 531; DB 9; Length 107;  
 Best Local Similarity 92.5%; Pred. No. 7.6e-37;  
 Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNWYQKPKAPKLLIFVSSNLHSGVPS 60  
 Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNWYQKPKAPKLLIFVSSNLHSGVPS 60  
 Qy 61 RFGSGSGTDYTLTISSLOPEDFATYYCQYSTVPWTFGGTKVEIK 107  
 Db 61 RFGSGSGTDYTLTISSLOPEDFATYYCQYSTVPWTFGGTKVEIK 107

RESULT 9

US-10-234-671-15  
 Sequence 15, Application US/10234671  
 Publication No. US20030190317A1  
 GENERAL INFORMATION:  
 APPLICANT: Baca, Manuel  
 Wells, James A.  
 Presta, Leonard G.  
 Lowman, Henry B.  
 Chen, Yvonne M.  
 TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
 NUMBER OF SEQUENCES: 131  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/234,671  
 FILING DATE: 03-Sep-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/056160

FILING DATE: 06-APR-1998  
 APPLICATION NUMBER: 60/126446  
 FILING DATE: 07-APR-1997  
 APPLICATION NUMBER: 60/054856  
 FILING DATE: 06-AUG-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cui, Steven X.  
 REGISTRATION NUMBER: 44,637  
 REFERENCE/DOCKET NUMBER: P1093R2C1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-8674  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 107 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
 US-10-234-671-15

Query Match 92.5%; Score 531; DB 14; Length 107;  
 Best Local Similarity 92.5%; Pred. No. 7.6e-37;  
 Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNWYQKPKAPKLLIFVSSNLHSGVPS 60  
 Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNWYQKPKAPKLLIFVSSNLHSGVPS 60  
 Qy 61 RFGSGSGTDYTLTISSLOPEDFATYYCQYSTVPWTFGGTKVEIK 107  
 Db 61 RFGSGSGTDYTLTISSLOPEDFATYYCQYSTVPWTFGGTKVEIK 107

RESULT 10

US-10-974-591-15  
 Sequence 15, Application US/10974591  
 Publication No. US20050112126A1  
 GENERAL INFORMATION:  
 APPLICANT: Baca, Manuel  
 Wells, James A.  
 Presta, Leonard G.  
 Lowman, Henry B.  
 Chen, Yvonne M.  
 TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
 NUMBER OF SEQUENCES: 131  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/974,591  
 FILING DATE: 26-Oct-2004  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/723752  
 FILING DATE: 27-NOV-2000  
 APPLICATION NUMBER: 08/908469  
 FILING DATE: 06-AUG-1997  
 APPLICATION NUMBER: 08/833504  
 FILING DATE: 07-APR-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cui, Steven X.  
 REGISTRATION NUMBER: 44,637  
 REFERENCE/DOCKET NUMBER: P1093PID1C1  
 TELECOMMUNICATION INFORMATION:

```
;
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-974-591-15

Query Match          92.5%; Score 531; DB 17; Length 107;
Best Local Similarity 92.5%; Pred. No. 7.6e-37;
Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYLNWYQKPGKAPKLLIYFTSSLNHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYLNWYQKPGKAPKLLIYFTSSLNHSGVPS 60
QY 61 RFSGSGSGTDYTLTISSLPEDPATYVYCHOYSKLPWTFGQGTKEIK 107
DB 61 RFSGSGSGTDYTLTISSLPEDPATYVYCHOYSKLPWTFGQGTKEIK 107

RESULT 11
US-09-056-160B-105
; Sequence 105, Application US/09056160B
; Patent No. US2002003231SA1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-Aug-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-160B-105

Query Match          92.3%; Score 530; DB 9; Length 110;
Best Local Similarity 90.7%; Pred. No. 9.4e-37;
Matches 98; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYLNWYQKPGKAPKLLIYFTSSLNHSGVPS 60
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DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYLNWYQKPGKAPKLLIYFTSSLNHSGVPS 60
QY 61 RFSGSGSGTDYTLTISSLPEDPATYVYCHOYSKLPWTFGQGTKEIKR 108
DB 61 RFSGSGSGTDYTLTISSLPEDPATYVYCHOYSKLPWTFGQGTKEIKR 108

RESULT 12
US-10-234-671-103
; Sequence 103, Application US/10234671
; Publication No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/056160
; FILING DATE: 06-Apr-1998
; APPLICATION NUMBER: 60/126446
; FILING DATE: 07-Apr-1997
; APPLICATION NUMBER: 60/054856
; FILING DATE: 06-Aug-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093R2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-234-671-103

Query Match          92.3%; Score 530; DB 14; Length 110;
Best Local Similarity 90.7%; Pred. No. 9.4e-37;
Matches 98; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYLNWYQKPGKAPKLLIYFTSSLNHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYLNWYQKPGKAPKLLIYFTSSLNHSGVPS 60
QY 61 RFSGSGSGTDYTLTISSLPEDPATYVYCHOYSKLPWTFGQGTKEIKR 108
DB 61 RFSGSGSGTDYTLTISSLPEDPATYVYCHOYSKLPWTFGQGTKEIKR 108

RESULT 13
US-10-974-591-103
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Query Match 92.2%; Score 529; DB 13; Length 108;  
Best Local Similarity 90.7%; Pred. No. 1.1e-36;  
Matches 98; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVPS 60  
Qy 61 RFSGGSGTDYTLTISSLQPEDFATYYCHQYKLPWTFQGGTKVEIKR 108  
Db 61 RFSGGSGTDFTLTISSLQPEDFATYYCQYSTVPWTFQGGTKVEIKR 108

Search completed: August 1, 2005, 09:28:00  
Job time : 29.4953 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 1, 2005, 08:58:15 ; Search time 6.11574 Seconds  
(without alignments)  
1699.125 Million cell updates/sec

Title: US-10-089-500-10

Perfect score: 574

Sequence: 1 DQMTQSPSSLSASVGRVT.....HOYSKLPWTFGGQTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79:\*

1: piri:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	496	86.4	108	1 K1HUHU	Ig kappa chain V-I
2	488	85.0	127	2 S40367	Ig kappa chain V-J
3	472	82.2	108	1 K1HURE	Ig kappa chain V-I
4	471	82.1	125	2 S40333	Ig kappa chain V-J
5	469	81.7	129	2 S52789	Ig kappa chain V r
6	468	81.5	123	2 S40331	Ig kappa chain - h
7	467	81.4	108	2 B49047	Ig kappa chain V r
8	466	81.2	110	2 S41118	Ig kappa chain V-J
9	466	81.2	111	2 A38740	Ig kappa chain V r
10	465	81.0	108	2 S44122	Ig kappa chain V r
11	464	80.8	111	2 E38740	Ig kappa chain V r
12	461	80.3	108	2 I39154	Ig kappa chain (BR
13	461	80.3	109	2 S31998	Ig kappa chain - h
14	460	80.1	107	2 S36264	Ig kappa chain V
15	459	80.0	108	1 K1HWE	Ig kappa chain V-I
16	459	80.0	111	2 G38740	Ig kappa chain V r
17	459	80.0	139	2 S40365	Ig kappa chain - h
18	458	79.8	131	2 S40352	Ig kappa chain V-J
19	457	79.6	129	2 S40369	Ig kappa chain - h
20	456	79.4	111	2 C38740	Ig kappa chain V r
21	455	79.3	108	2 S19674	Ig kappa chain V r
22	455	79.3	141	2 A49134	Ig kappa chain V-I
23	454	79.1	108	1 K1HURY	Ig kappa chain V-I
24	453.5	79.0	107	2 S36275	Ig kappa chain V-I
25	453	78.9	107	2 B49026	Ig kappa chain V r
26	453	78.9	108	1 K1HUAG	Ig kappa chain V-I
27	453	78.9	109	2 S31981	Ig kappa chain - h
28	452.5	78.8	124	2 S40336	Ig kappa chain V-J
29	451	78.6	135	2 S24320	Ig kappa chain pre

30	450	78.4	108	1 K1HUHU	Ig kappa chain V-I
31	449.5	78.3	106	2 KC2397	anti-tetanus toxin
32	448	78.0	108	1 KWMS73	Ig kappa chain V r
33	447	77.9	117	2 S46371	Ig kappa chain V-J
34	446	77.7	108	1 K1HUKA	Ig kappa chain V-I
35	446	77.7	125	2 S40349	Ig kappa chain V-J
36	445.5	77.6	125	2 S40315	Ig kappa chain - h
37	445	77.5	108	1 K1HUBN	Ig kappa chain V-I
38	445	77.5	108	1 K1HULY	Ig kappa chain V-I
39	445	77.5	122	2 S40370	Ig kappa chain - h
40	445	77.5	129	2 S52793	Ig kappa chain V r
41	445	77.5	132	2 S40334	Ig kappa chain - h
42	444	77.4	108	2 S47182	Ig kappa chain - h
43	444	77.4	117	2 S46376	Ig kappa chain V-J
44	444	77.4	122	2 S40314	Ig kappa chain - h
45	443	77.2	108	1 K1HUBI	Ig kappa chain V-I
46	443	77.2	129	2 S40317	Ig kappa chain - h
47	442	77.0	108	1 K1HUUU	Ig kappa chain V-I
48	442	77.0	120	2 S46370	Ig kappa chain V-J
49	442	77.0	129	1 K1HUMK	Ig kappa chain pre
50	442	77.0	130	2 S40368	Ig kappa chain - h
51	441	76.8	108	2 S69900	Ig kappa chain (cl
52	441	76.8	126	2 S40335	Ig kappa chain V-J
53	441	76.8	128	2 S46372	Ig lighc chain var
54	440	76.7	107	2 S36269	Ig lambda chain V
55	439	76.5	107	2 JLO139	Ig kappa chain V r
56	439	76.5	107	2 I69017	anti-Hiv1 envelope
57	439	76.5	124	2 S40318	Ig kappa chain V r
58	438	76.3	108	1 K1HUGL	Ig kappa chain V-I
59	437	76.1	108	1 K1HUDE	Ig kappa chain V-I
60	437	76.1	125	2 S40316	Ig kappa chain - h
61	436	76.0	108	1 K1HUSW	Ig kappa chain V-I
62	436	76.0	109	2 S31978	Ig kappa chain - h
63	436	76.0	129	2 S52792	Ig kappa chain V r
64	436	76.0	132	2 S38646	Ig kappa chain V r
65	435	75.8	123	2 S40313	Ig kappa chain V-J
66	435	75.8	125	2 S40350	Ig kappa chain - h
67	434.5	75.7	107	1 K1HUAR	Ig kappa chain V-I
68	434	75.6	107	2 S36262	Ig lambda chain V
69	434	75.6	117	2 S42263	Ig kappa chain V r
70	434	75.6	117	2 S43528	Ig kappa chain V r
71	434	75.6	122	2 A29380	Ig kappa chain pre
72	434	75.6	125	2 S40353	Ig kappa chain V-J
73	433	75.4	108	1 K1HUKU	Ig kappa chain V-I
74	433	75.4	109	2 S31979	Ig kappa chain - h
75	432	75.3	108	1 K1HUMS	Ig kappa chain V-I
76	432	75.3	108	2 S69903	Ig kappa chain (cl
77	432	75.3	115	2 JLO080	Ig kappa chain pre
78	431.5	75.2	109	1 K1HUMV	Ig kappa chain V-I
79	430	74.9	108	2 S36279	Ig lambda chain V
80	429	74.7	109	2 S31980	Ig kappa chain - h
81	428	74.6	95	2 PH0862	Ig kappa chain V r
82	428	74.6	108	1 KWMSAR	Ig kappa chain V r
83	428	74.6	108	2 S31977	Ig kappa chain - h
84	427.5	74.5	108	2 S30521	Ig kappa chain V r
85	427	74.4	95	2 PH0864	Ig kappa chain V r
86	427	74.4	107	2 A48677	Ig kappa chain V-J
87	427	74.4	108	2 S69902	Ig kappa chain (cl
88	427	74.4	109	2 PH0888	Ig kappa chain V r
89	427	74.4	110	2 PN0535	Ig kappa chain V r
90	427	74.4	126	2 A34904	Ig kappa chain pre
91	427	74.4	127	2 S11240	Ig kappa chain V r
92	426	74.2	108	1 K1HUEU	Ig kappa chain V-I
93	426	74.2	109	2 S32001	Ig kappa chain - h
94	426	74.2	124	2 S40348	Ig kappa chain V-J
95	425.5	74.1	107	2 S47183	Ig kappa chain - h
96	425	74.0	108	2 S36277	Ig lambda chain V
97	424	73.9	107	2 B48677	Ig kappa chain V-J
98	424	73.9	128	2 B26406	Ig kappa chain V r
99	423.5	73.8	107	2 S69901	Ig kappa chain (cl
100	423.5	73.8	108	2 S34007	Ig kappa chain V r





A;Cross-references: EMBL:X72443; NID:g441354; PIDN:CAA51111.1; PID:g441355  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;34-108/Domain: immunoglobulin homology <IMM>

Query Match 82.18; Score 471; DB 2; Length 125;  
Best Local Similarity 82.24; Pred. No. 1e-34;  
Matches 88; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVSGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFVSSNLHSGVPS 60  
DB 19 DIQMTQSPSTLSASVSGDRVTITCRASQSISSWLAWYQKPGKAPKLLIYKASLESQVPS 78  
QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYKSLPWTFGGQTKVEIK 107  
DB 79 RFGSGSGTEFTLTISLQPDPAFYCCQYNSYPWTFGGQTKVEIK 125

RESULT 5  
S52789  
IG kappa chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C;Accession: S52789  
R;Rocca, A.; Khamlich, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret,  
submitted to the EMBL Data Library, March 1995  
A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-  
A;Reference number: S52789  
A;Accession: S52789  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-129 <ROC>  
A;Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match 81.74; Score 469; DB 2; Length 129;  
Best Local Similarity 84.14; Pred. No. 1.6e-34;  
Matches 90; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVSGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFVSSNLHSGVPS 60  
DB 23 DIQMTQSPSSLSASVSGDRVTITCSASQDISNYLNWYQKPGKAPKLLIHAASLETGVP 82  
QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYKSLPWTFGGQTKVEIK 107  
DB 83 RFGSGSGTEFTLTISLQPDPAFYCCQYDNLPLTFGGQTKVEIK 129

RESULT 6  
S40331  
IG kappa chain - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S40331  
R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40331; MUID:94080891; PMID:8258341  
A;Accession: S40331  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-123 <KLE>  
A;Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PID:g441351  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;32-106/Domain: immunoglobulin homology <IMM>

Query Match 81.58; Score 468; DB 2; Length 123;  
Best Local Similarity 85.04; Pred. No. 1.8e-34;  
Matches 91; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVSGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFVSSNLHSGVPS 60  
DB 17 DIQMTQSPSSLSASVSGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQVPS 76  
QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYKSLPWTFGGQTKVEIK 107  
DB 77 RFGSGSGTEFTLTISLQPDPAFYCCQYNSYPWTFGGQTKVEIK 123

RESULT 7  
B49047  
IG kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: B49047  
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.  
Eur. J. Immunol. 22, 2231-2236, 1992  
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes  
A;Reference number: A49047; MUID:92387224; PMID:1516616  
A;Accession: B49047  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-108 <VIC>  
A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77  
A;Experimental source: thymic B lymphocytes  
A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBI:113209)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.44; Score 467; DB 2; Length 108;  
Best Local Similarity 84.34; Pred. No. 2e-34;  
Matches 91; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVSGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFVSSNLHSGVPS 60  
DB 1 DIQMTQSPSSLSASVSGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQVPS 60  
QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYKSLPWTFGGQTKVEIKR 108  
DB 61 RFGSGSGTEFTLTISLQPDPAFYCCQYNSYPWTFGGQTKVEIKR 108

RESULT 8  
S44118  
IG kappa chain V-J region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C;Accession: S44118  
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable re-

A;Reference number: S44105  
A;Accession: S44118  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-110 <HAW>  
A;Cross-references: EMBL:X31395; NID:g472972; PIDN:CAA83270.1; PID:g940529  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.24; Score 466; DB 2; Length 110;  
Best Local Similarity 82.74; Pred. No. 2.5e-34;  
Matches 91; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 1 DIQMTQSPSSLSASVSGDRVTITCSASQDISNYLNWYQKPGKAPKLLIFVSSNLHSGVPS 60  
DB 1 DIQMTQSPSSLSASVSGDRVTITCSASQDISNYLNWYQKPGKAPKLLIYDASNLGTGVP 60  
QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYKSLP--WTFGGQTKVEIKR 108  
DB 61 RFGSGSGTEFTLTISLQPDPAFYCCQYDNLPGVTFPGGQTKVDIKR 110

```
RESULT 9
A38740
Ig kappa chain V region (Py20) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C:Accession: A38740
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: A38740
A:Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match      81.2%; Score 466; DB 2; Length 111;
Best Local Similarity 79.6%; Pred. No. 2.5e-34;
Matches 86; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLHSGVPS 60
Db 4 DVQMTQTSSLSASLGDRVTITCSASQGISNYLNWYQKPGDGTVKLLIYTSLSHSGVPS 63

QY 61 RFGSGSGTDYTLTISSLOPEDPATYCHQYSKLPWTFGQGTKEIKR 108
Db 64 RFGSGSGTDYSLTISNLEPEDVATYCCQYQYKVPWTFGGKLEIKR 111

RESULT 10
S44122
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A:Description: Idiotype vaccination against human B-cell lymphoma: rescue of variable H
A:Reference number: S44105
A:Accession: S44122
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-108 <HAW>
A:Cross-references: EMBL:Z31390; NID:G472976; PIDN:CAA83265.1; PID:G940533
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      81.0%; Score 465; DB 2; Length 108;
Best Local Similarity 83.3%; Pred. No. 3e-34;
Matches 90; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKLGKAPKLLIYSASSLSQSGVPS 60

QY 61 RFGSGSGTDYTLTISSLOPEDPATYCHQYSKLPWTFGQGTKEIKR 108
Db 61 TFGSGSGGTDYTLTISSLOPEDPATYCCQYQYKVPWTFGGKLEIKR 108

RESULT 11
E38740
Ig kappa chain V region (Py54) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C:Accession: E38740
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
```

```
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: E38740
A:Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match      80.8%; Score 464; DB 2; Length 111;
Best Local Similarity 79.6%; Pred. No. 3.7e-34;
Matches 86; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLHSGVPS 60
Db 4 DVQMTQTSSLSASLGDRVTITCSASQGISNYLNWYQKPGDGTVKLLIYTSLSHSGVPS 63

QY 61 RFGSGSGTDYTLTISSLOPEDPATYCHQYSKLPWTFGQGTKEIKR 108
Db 64 RFGSGSGTDYSLTISDLEPDATYCCQYQYKVPWTFGGKLEIKR 111

RESULT 12
I39154
Ig kappa chain (BRE) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C:Accession: I39154
R:Schormann, N.; Murrell, J.R.; Liepnieks, J.J.; Benson, M.D.
Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
A:Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A proposed
A:Reference number: I39154; MUID:96003804; PMID:7568160
A:Accession: I39154
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-108 <RES>
A:Cross-references: EMBL:U31344; NID:G944925; PIDN:AAA79238.1; PID:G944926
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      80.3%; Score 461; DB 2; Length 108;
Best Local Similarity 82.4%; Pred. No. 6.7e-34;
Matches 89; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISDYLIWYQKLGKAPNLLIYDASTLTSTGVPS 60

QY 61 RFGSGSGTDYTLTISSLOPEDPATYCHQYSKLPWTFGQGTKEIKR 108
Db 61 RFGSGSGTGTFTTISSLOPEDATYCCQYQYKVPWTFGGKLEIKR 108

RESULT 13
S31998
Ig kappa chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S31998
R:Fortolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A:Reference number: S31977
A:Accession: S31998
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-109 <POR>
A:Cross-references: EMBL:Z15081; NID:G38501; PIDN:CAA78790.1; PID:G38502
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
```

```

Query Match      80.0%; Score 459; DB 1; Length 108;
Best Local Similarity 80.6%; Pred.No.le-33;
Matches 87; Conservative 13; Indels 0; Gaps 0;
1 DIOMTOSPSLSASVGDRTVITCSAODISINLWYOOKPGKPKLIIFYSNLSHGVP 60

```

Qy	1	DIOMTQSPSSLASVSGDVRVITITCSAODISNYLNTWYQOKEGKAPKLLIIPVSSNLIHSGVPS	60
Db	1	DIOMTQSPSSLASVSGDVRVITITCRASGGIRNDITWYQOKEGTPAPRLIYIGATISLQSGVPS	60
Qy	61	RFSGGSGTDYTLITLISLQPEDFATYVCHQYKLPMTFGGQTKVEIKR	108
Db	61	RFSGGSGTGIEFTLITLINSLOPEDFATYVCLQYSGFPMTFGGQTKVEIKR	108

Search completed: August 1, 2005, 09:18:42  
Job time : 8.11574 secs

RESULT 14

Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
 C:Accession: S36264  
 R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
 EMBO J. 12, 725-734, 1993  
 A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
 A:Reference number: S36256; MUID:93178448; PMID:7679990  
 A:Accession: S36264  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-107 <GR1>  
 A:Cross-references: EMBL:Z18845; NID:g33426; PIDN:CAA79297.1; PID:g939919  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F16-90/Domain: immunoglobulin homology <IMW>

Query Match 80.1%; Score 460; DB 2; Length 107;  
Best Local Similarity 82.2%; Pred. No. 8.1e-34;  
Matches 88; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy	1	DIQWTQPSSLSASVGDRVITTC	SASQDISNYLNWYQQKPGKAPKLIIFYSSNLHSGVPS	60
	:	: : : : : : : : : : : :	: : : : : : : : : : : :	
Db	1	EIVLTQPSSLSASVGDRVITTC	RASQSISSYLNWYQQKPGKAPKLIIYAASSLQSGVPS	60

```

61 RFSGGSGTDYTLTISSLQPEDFATYYCHQYSKLPWTFGGTKVEIK 107
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 RFSGGSGTDFTLISSLQPEDFATYYCOYSNYPFTFGGTKVDIK 107

```

## RESULT 15

K1HWE  
 I9 kappa chain V-I region (WEA) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 09-Jul-2004  
 C:Accession: A01876  
 R:Goni, F.; Frangione, B.  
 Proc. Natl. Acad. Sci. U.S.A. 80. 4837-4841, 1983  
 A:Title: Amino acid sequence of the Fv region of a human monoclonal IGM (protein WEA) with  
 A:Reference number: A93964; MUID:83273707; PMID:6410398  
 A:Accession: A01876  
 A:Molecule type: protein  
 A:Residues: 1-108 <GON>  
 A:Cross-references: UNIPROT:P01610  
 C:Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated galactose.  
 C:Genetics:  
 A:Gene: GDB:IGKV1  
 A:Cross-references: GDB:i36264  
 A:Map position: 2p12-2p12  
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) and two identical heavy (lambda) chain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into larger oligomers.  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer  
 F:16-90/Domain: immunoglobulin homology <IMM>  
 F:23-88/Disulfide bonds: #status predicted

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:55 ; Search time 28.0249 Seconds  
(without alignments)  
1973.408 Million cell updates/sec

Title: US-10-089-500-10

Perfect score: 574

Sequence: 1 DIQMTQSPSSLSASVGRVT.....HOYSKLPWTFGQTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	496	86.4	108	1	KV1B_HUMAN
2	472	82.2	108	1	KV1O_HUMAN
3	471	82.1	108	2	Q9UL77
4	465	81.0	236	2	Q6GMW1
5	459.5	80.1	107	2	Q96SA9
6	459	80.0	108	1	KV1R_HUMAN
7	456	79.4	236	2	Q723Y4
8	454	79.1	108	1	KV1P_HUMAN
9	453	78.9	108	1	KV1A_HUMAN
10	453	78.9	236	2	Q6GMX8
11	452	78.7	108	1	KV1Y_HUMAN
12	450	78.4	108	1	KV1V_HUMAN
13	450	78.4	108	2	Q9UL70
14	449	78.2	236	2	Q6GMX0
15	448	78.0	108	1	KV5J_MOUSE
16	448	78.0	236	2	Q6GMX9
17	446	77.7	108	1	KV1K_HUMAN
18	445	77.5	108	1	KV1M_HUMAN
19	445	77.5	108	1	KV1V_HUMAN
20	443	77.2	108	1	KV1C_HUMAN
21	442.5	77.1	107	2	Q9UL81
22	442	77.0	108	1	KV1N_HUMAN
23	442	77.0	116	2	Q96FF6
24	442	77.0	129	1	KV1W_HUMAN
25	440	76.7	236	2	Q6PIH7
26	439	76.5	244	2	Q65ZC8
27	438	76.3	108	1	KV1G_HUMAN
28	437	76.1	108	1	KV1E_HUMAN
29	437	76.1	234	2	Q7Z473
30	436	76.0	108	1	KV1Q_HUMAN
31	434.5	75.7	107	1	KV1D_HUMAN

ALIGNMENTS

32	434	75.6	240	2	Q65ZC9	Q65zc9 homo sapien
33	433	75.4	108	1	KV1L_HUMAN	P01604 homo sapien
34	432	75.3	108	1	KV1S_HUMAN	P01601 homo sapien
35	431.5	75.2	109	1	KV1T_HUMAN	P01612 homo sapien
36	429	74.7	108	2	Q9UL79	Q9ul79 homo sapien
37	428	74.6	108	1	KV5K_MOUSE	P01644 mus musculus
38	427	74.4	108	1	KV5L_MOUSE	P01645 mus musculus
39	427	74.4	108	1	KV5M_MOUSE	P01646 mus musculus
40	426	74.2	108	1	KV1F_HUMAN	P01598 homo sapien
41	425	74.0	108	1	KV5O_MOUSE	P01648 mus musculus
42	423	73.7	108	1	KV5N_MOUSE	P01647 mus musculus
43	420	73.2	236	2	Q6PIH4	O6pih4 homo sapien
44	420	73.2	236	2	Q6PIH5	O6pih5 homo sapien
45	417	72.6	108	1	KV5U_MOUSE	Q94946 mus musculus
46	416	72.5	107	2	Q9JL84	Q9jl84 mus musculus
47	414	72.1	129	1	KV1X_HUMAN	P04432 homo sapien
48	409	71.3	134	1	KV4C_HUMAN	P06314 homo sapien
49	400	69.7	108	1	KV5S_MOUSE	P01652 mus musculus
50	399	69.5	109	2	Q920E6	Q920e6 mus musculus
51	397	69.2	117	1	KV1J_HUMAN	P01602 homo sapien
52	395	68.8	236	2	Q7TS98	Q7ts98 mus musculus
53	394	68.6	117	1	KV1I_HUMAN	P01601 homo sapien
54	391	68.1	108	1	KV5Q_MOUSE	P01650 mus musculus
55	388.5	67.7	112	1	KV1U_HUMAN	P01613 homo sapien
56	387	67.4	114	1	KV4A_HUMAN	P18136 homo sapien
57	386	67.2	108	1	KV5P_MOUSE	P01625 homo sapien
58	385	67.1	108	1	KV5T_MOUSE	P01649 mus musculus
59	384	66.9	128	1	KV5E_MOUSE	P01653 mus musculus
60	383	66.7	298	2	Q9QTF0	P01637 mus musculus
61	381.5	66.5	109	1	KV3D_HUMAN	Q9qvfo synthetic c
62	381	66.4	130	1	KV5G_MOUSE	P01622 homo sapien
63	380	66.2	108	1	KV5R_MOUSE	P01639 mus musculus
64	379.5	66.1	109	1	KV3B_HUMAN	P01651 mus musculus
65	379.5	66.1	109	1	KV3E_HUMAN	P01620 homo sapien
66	379.5	66.1	109	1	KV3F_HUMAN	P01623 homo sapien
67	379.5	66.1	129	1	KV3H_HUMAN	P04207 homo sapien
68	378.5	65.9	133	1	KV3L_HUMAN	P18135 homo sapien
69	378.5	65.9	133	1	KV4B_HUMAN	P06313 homo sapien
70	377	65.7	108	1	KV5D_MOUSE	P01636 mus musculus
71	376.5	65.6	110	1	KV3P_MOUSE	P01668 mus musculus
72	376.5	65.6	243	2	Q7TQM2	Q7tqm2 mus musculus
73	375	65.3	111	1	KV3O_MOUSE	P01667 mus musculus
74	375	65.3	111	1	KV3Q_MOUSE	P01669 mus musculus
75	374.5	65.2	134	2	Q8VDD0	Q8vdd0 mus musculus
76	372	64.8	108	2	Q9UL83	Q9ul83 homo sapien
77	372	64.8	238	2	Q66JS7	Q66js7 mus musculus
78	369.5	64.4	109	1	KV3F_HUMAN	P01624 homo sapien
79	369.5	64.4	112	2	Q8K1F3	Q8k1f3 mus musculus
80	366.5	63.9	109	2	Q9UL78	Q9ul78 homo sapien
81	365.5	63.7	235	2	Q6FJF2	O6pfj2 homo sapien
82	365	63.6	111	1	KV3M_MOUSE	P01665 mus musculus
83	365	63.6	149	1	KV5A_MOUSE	P01633 mus musculus
84	364.5	63.5	114	2	Q8K1F1	Q8k1f1 mus musculus
85	364.5	63.5	235	2	Q6GMW0	Q6gmw0 homo sapien
86	363	63.0	108	2	Q8K1J0	Q8k1j0 mus musculus
87	361.5	63.0	112	2	Q8K1F2	Q8k1f2 mus musculus
88	361	62.9	111	1	KV3L_MOUSE	P01664 mus musculus
89	361	62.9	111	2	Q920E9	Q920e9 mus musculus
90	360.5	62.8	109	2	Q9UL85	Q9ul85 homo sapien
91	359	62.5	111	1	KV3N_MOUSE	P01666 mus musculus
92	357.5	62.3	108	1	KV3A_HUMAN	P01619 homo sapien
93	357	62.2	128	1	KV3K_HUMAN	P06311 homo sapien
94	357	62.2	487	2	Q65ZL2	Q65z12 mus sp. fv/
95	356	62.0	111	1	KV3R_MOUSE	P01670 mus musculus
96	356	62.0	111	1	KV3S_MOUSE	P01671 mus musculus
97	356	62.0	127	2	Q925S9	Q925s9 mus musculus
98	356	62.0	131	1	KV3I_MOUSE	P01661 mus musculus
99	355	61.8	136	1	KV5B_MOUSE	P01634 mus musculus
100	354	61.7	109	1	KV4D_HUMAN	P83593 homo sapien

```
RESULT 1
KV1B HUMAN
ID KV1B HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=72189444; PubMed=5028201;
RX Schiechl H., Hilschmann N.;
RA "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=7022433; PubMed=1234024;
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the Bence-
RT Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -!- MISCELLANEOUS: The structure of the V region was determined by
CC molecular replacement methods using the known structure of the V
CC region of the kappa chain REI.
CC -!- MISCELLANEOUS: This C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91653; KIHUAU.
DR PDB; 1JY5; X-ray; A=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT STRAND 1 23
FT TURN 24 34
FT STRAND 35 49
FT TURN 50 56
FT STRAND 57 88
FT TURN 89 97
FT STRAND 98 107
FT DISULFID 23 88
FT STRAND 4 5
FT STRAND 10 12
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT STRAND 60 61
FT TURN 62 67
FT STRAND 68 69
FT TURN 70 75
FT STRAND 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
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FT NON TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187BE6F6FB9 CRC64;
Query Match 86.4%; Score 496; DB 1; Length 108;
Best Local Similarity 87.0%; Pred. No. 1.9e-43;
Matches 94; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 1 DIQWTQSPSSLSASVGDRTVITCSASQDISNLYNWYQQKPGKAPKLLIFYSNLSHGVP 60
DB 1 DIQWTQSPSSLSASVGDRTVITCSASQDISNLYNWYQQKPGKAPKLLIFYSNLSHGVP 60
QY 61 RFSGGSGTDTLTITSSSQDEFTATYCHQYSKLPWTGQGTQKVEIKR 108
DB 61 RFSGGSGAHTFTTSSSQDEFTATYCHQYSKLPWTGQGTQKVEIKR 108
RESULT 2
KV1O HUMAN
ID KV1O HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region Rei.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=7603968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91663; KIHURE.
DR PDB; 1AR2; X-ray; @=1-107.
DR PDB; 1BWW; X-ray; A/B=1-107.
DR PDB; 1REI; X-ray; A/B=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT STRAND 24 34
FT TURN 35 49
FT STRAND 50 56
FT TURN 57 88
FT STRAND 89 97
FT TURN 98 107
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
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FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match
Best Local Similarity 82.4%; Score 472; DB 1; Length 108;
Matches 89; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQWTSPLSLASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
Db 1 DIQWTSPLSLASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYEASNLQAGVPS 60

QY 61 RFGSGSGTDYTLTISLQPEDPATYCHQYKLPWTFGGTKVEIKR 108
Db 61 RFGSGSGTDYTLTISLQPEDPATYCHQYKLPWTFGGTKLQITR 108

RESULT 3
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
TISSUE=Spleen;
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
[1]
SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSP; P01607; IHW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 108 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match
Best Local Similarity 82.1%; Score 471; DB 2; Length 108;
Matches 90; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQWTSPLSLASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
Db 1 DIQWTSPLSLASVGDRTVITCSASQDISNYLNWYQKPGKAPNLLIYAASSLQSGVPS 60
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QY 61 RFGSGSGTDYTLTISLQPEDPATYCHQYKLPWTFGGTKVEIKR 108
Db 61 RFGSGSGTDYTLTISLQPEDPATYCHQYKLPWTFGGTKVEIKR 108

RESULT 4
Q6GMW1 PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszynski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
SEQUENCE FROM N.A.
TISSUE=Spleen;
Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Query Match
Best Local Similarity 81.0%; Score 465; DB 2; Length 236;
Matches 91; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 2 IQWTSPLSLASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 61
Db 24 IQWTSPLSLASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIYAASSLQSGVPS 83

QY 62 RFGSGSGTDYTLTISLQPEDPATYCHQYKLPWTFGGTKVEIKR 108
Db 62 RFGSGSGTDYTLTISLQPEDPATYCHQYKLPWTFGGTKVEIKR 108
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Db 84 FSGSGGTDTLTITSSLPEDFATYCYLQDYNYPWTFGQTKVEIKR 130
RESULT 5
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-WAR-2004 (TREMELrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSSP; P01607; LBWW.
DR InterPro; IPR007110; Ig-like.
DR SMART; IPR003596; Ig_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 80.1%; Score 459.5; DB 2; Length 107;
Best Local Similarity 85.3%; Pred. No. 1.1e-39;
Matches 93; Conservative 5; Mismatches 8; Indels 3; Gaps 2;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNVLNMYQQKPGKAPKLLIPYSNLSHGVP 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQISSYLVNMYQQKPGKAPKLLIYAASLSQGV 60
QY 61 RFSGSGGTDTLTITSSLPEDFATYCHQ-YSKLPWTFGQTKVEIKR 108
Db 61 RFSGSGGTDTLTITSSLPEDFATYCYQSYSTL--TFGGTKVEIKR 107

RESULT 6
KVIR_HUMAN STANDARD; PRT; 108 AA.
AC F01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region WEA.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated galactose
RT in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
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CC -! MISCELLANEOUS: This chain was obtained from a monoclonal antibody
CC against 3,4-pyruvylated galactose and isolated from a patient with
CC Waldenstrom's macroglobulinemia.
DR PIR; A01876; KIHUME.
DR HSSP; P80362; LWTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Monoclonal antibody.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match 80.0%; Score 459; DB 1; Length 108;
Best Local Similarity 80.6%; Pred. No. 1.2e-39;
Matches 87; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNVLNMYQQKPGKAPKLLIPYSNLSHGVP 60
Db 1 DIQMTQSPSSLSASVGRVTITCSAQIRNDLTWYQQKPGTAPKRLIYGATSLQSGVP 60
QY 61 RFSGSGGTDTLTITSSLPEDFATYCHQYKSLPWFQGGTKVEIKR 108
Db 61 RFSGSGGTDTLTITSSLPEDFATYCYLQSYSPWTFGQTKVEIKR 108

RESULT 7
Q723Y4 PRELIMINARY; PRT; 236 AA.
AC Q723Y4;
DT 01-OCT-2003 (TREMELrel. 25, Created)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-WAR-2004 (TREMELrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Bosak S.A., McQuellan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
```



and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

SEQUENCE FROM N.A.  
TISSUE=Skeletal Muscle;  
Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
EMBL; BC005332; AA05332.1; -;  
HSSP; P01834; 1HEZ.  
InterPro; IPR007110; Ig-like.  
InterPro; IPR003597; Ig cl.  
InterPro; IPR003006; Ig\_MHC.  
InterPro; IPR003596; Ig\_v.  
Pfam; PF07654; Cl-Bet; 1.  
SMART; SM00406; IGV; 1.  
PROSITE; PS00835; IG\_LIKE; 2.  
Hypothetical protein\_MHC; UNKNOWN\_1.  
SEQUENCE 236 AA; 25702 MW; 7BFBE4ED23084BC6 CRC64;

Query Match 79.4%; Score 456; DB 2; Length 236;  
Best Local Similarity 81.5%; Pred. No. 6.3e-39;  
Matches 88; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPGKAPKLLIFVSSNLHSGVPS 60  
Db 23 DIQMTQSPSSLSASVGRVTITCRASQDISNYLAWFOQKPGKAPKSLIYGASSLQSGVQS 82

Qy 61 RFSGGSGTDYTLTISSLOPEDPATYCHQYSKLPWTFGGTKVEIKR 108  
Db 83 KFSGSGSGTDFTLTISLQPEDPATYCCQYKSPVTFGGTKLEIKR 130

## RESULT 8

KVLP\_HUMAN STANDARD; PRT; 108 AA.

AC P01608;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-I region Roy.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=68362076; PubMed=5595110;  
RA Hilschmann N.;  
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Cum.)";  
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080 (1967).  
RN [2]  
RP REVISIONS TO 39 AND 41.  
RA Hilschmann N., Barnikol H.U., Hees M., Langer B., Ponstingl H.,  
RA Steinmetz-Kayne M., Suter L., Watanabe S.;  
RL (In) Franek F., Shugar D. (eds.);  
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).  
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2) marker.  
CC PIR; A91638; KIHURY.  
DR HSSP; P01607; 1BMW.

DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Bence-Jones protein; Direct protein sequencing;

## Immunoglobulin V region.

KW DOMAIN 1 23 Framework-1.  
FT DOMAIN 24 34 Complementarity-determining-1.  
FT DOMAIN 35 49 Framework-2.  
FT DOMAIN 50 56 Complementarity-determining-2.  
FT DOMAIN 57 88 Framework-3.  
FT DOMAIN 89 97 Complementarity-determining-3.  
FT DOMAIN 98 107 Framework-4.  
FT DISULFID 23 88 By similarity.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11782 MW; PSACEDBSA313DF3A CRC64;

Query Match 79.1%; Score 454; DB 1; Length 108;  
Best Local Similarity 80.6%; Pred. No. 4.1e-39;  
Matches 87; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPGKAPKLLIFVSSNLHSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISIFLNWYQOKPGKAPKLLIYDASKLEAGVPS 60

Qy 61 RFSGGSGTDYTLTISSLOPEDPATYCHQYSKLPWTFGGTKVEIKR 108  
Db 61 RFSGTSGTDFTLTISLQPEDPATYCCQFDNLPLTFGGTKVDPR 108

## RESULT 9

KVIA\_HUMAN STANDARD; PRT; 108 AA.

AC P01533;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-I region AG.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=69234734; PubMed=4893682;  
RA Titani K., Shinoda T., Putnam F.W.;  
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";  
RL J. Biol. Chem. 244:3550-3560 (1969).  
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
DR PIR; A01861; KIHUAG.  
DR HSSP; P01607; 1BMW.

DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.

KW Bence-Jones protein; Direct protein sequencing;  
KW Immunoglobulin V region.

FT DOMAIN 1 23 Framework-1.  
FT DOMAIN 24 34 Complementarity-determining-1.  
FT DOMAIN 35 49 Framework-2.  
FT DOMAIN 50 56 Complementarity-determining-2.  
FT DOMAIN 57 88 Framework-3.  
FT DOMAIN 89 97 Complementarity-determining-3.  
FT DOMAIN 98 107 Framework-4.  
FT DISULFID 23 88  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 78.9%; Score 453; DB 1; Length 108;  
Best Local Similarity 79.6%; Pred. No. 5.2e-39;  
Matches 86; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

```
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISINLYNWYQKPGKAPKLLIFYSNLSHGVPVS 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISINLYNWYQKPGKAPKLLIYDASNLSHGVPVS 60
QY 61 RFSGSGSGTDYTLTISSLPEDFATYYCHQYKLPWTFCQGTKEIKR 108
Db 61 RFSGSGSGTDFTITISGLQPEDIAITYCQYQDTLPRTFQGTKEIKR 108

RESULT 10
Q6GMX8 PRELIMINARY; PRT; 236 AA.
AC O6GMX8;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marushina K., Fawcett A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC073764; AAH3764.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match 78.9%; Score 453; DB 2; Length 236;
Best Local Similarity 80.6%; Pred. No. 1.3e-38;
Matches 87; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISINLYNWYQKPGKAPKLLIFYSNLSHGVPVS 60
Db 23 DIQMTQSPSSLSASVGRVTITCSASQDISINLYNWYQKPGKAPKLLIYAASLSHGVPVS 82
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QY 61 RFSGSGSGTDYTLTISSLPEDFATYYCHQYKLPWTFCQGTKEIKR 108
Db 83 RFSGSGSGTDFTITISGLQPEDFATYYCQAHSPFTFGPGTKVDIKR 130

RESULT 11
KVLY_HUMAN STANDARD; PRT; 108 AA.
ID KVLY_HUMAN AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-L region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
structural origin of altered domain interactions in immunoglobulin
light-chain dimers.";
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-
related fragment of the human KI Bence Jones protein Wat.";
RL J. Mol. Biol. 147:185-193(1981).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PDB; 1WTL; X-ray; A/B=1-108.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 BY similarity.
FT CONFLICT 30 31 TN -> SD (in Ref. 2).
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT STRAND 40 41
FT TURN 45 49
FT STRAND 50 52
FT TURN 53 54
FT STRAND 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
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FT	STRAND	98	98
FT	STRAND	102	106
FT	NON TER	108	108
SQ	SEQUENCE	108 AA;	D9D941B3F0FAE697 CRC64;
Query Match 78.7%; Score 452; DB 1; Length 108; Best Local Similarity 78.7%; Pred. No. 6.6e-39; Matches 85; Conservative 11; Mismatches 12; Indels 0; Gaps 0;			
Qy	1	DIQWTQSPSSLSASVGRDVITTCASODISNLYNWYQQKPKGAPKLIFYYSSNLHSGVPS	60
Db	1	DIQWTQSPSSLSASVGRDVITTCRASODIINYNNWFQORFGQAPKVLIYGASILETGVP	60
Qy	61	RFSGGSGTDYTLTISSQLQPEDFATYICYHQYSKLPWTFGGGTKEIKR	108
Db	61	RFSGGSGTDTFTTISSQLQEDIATYYCQYVDTLPLTFGGGTKEIDKR	108
<p>RESULT 12 KV1H HUMAN STANDARD; PRT; 108 AA.</p> <p>ID AC P01600; DT 21-JUL-1986 (Rel. 01, Created) DT 21-JUL-1986 (Rel. 01, Last sequence update) DT 23-OCT-2004 (Rel. 45, Last annotation update) DE IG kappa chain V-I region Hau. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. OX NCBI_TaxID=9606; RN [1] RP SEQUENCE. RX MEDLINE=71032830; PubMed=4097974; RA Watanabe S., Hilechmann N.; RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau) : subdivision within RT subgroups."; RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970). RC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker. CC -I- MISCELLANEOUS: This is a Bence-Jones protein. DR PIR; A01868; KIHUHU. DR PDB; 1P6L; X-ray; L=1-108. DR GO; GO:0005576; C:extracellular; NAS. DR GO; GO:0003823; F:antigen binding; NAS. DR GO; GO:0006955; P:immune response; NAS. DR InterPro; IPR007110; Ig-like. DR InterPro; IPR003596; Ig_v. DR Pfam; PF00047; Ig; 1. DR SMART; SM00406; IGV; 1. DR PROSITE; PSS0835; IG_LIKE; 1. KW 3D-structure; Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region. KW DOMAIN 1 23 Framework-1. FT DOMAIN 24 34 Complementarity-determining-1. FT DOMAIN 35 49 Framework-2. FT DOMAIN 50 56 Complementarity-determining-2. FT DOMAIN 57 88 Framework-3. FT DOMAIN 89 97 Complementarity-determining-3. FT DOMAIN 98 107 Framework-4. FT DISULPID 23 88 By similarity. FT NON TER 108 108 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;</p>			
Query Match 78.4%; Score 450; DB 1; Length 108; Best Local Similarity 80.6%; Pred. No. 1.1e-38; Matches 87; Conservative 10; Mismatches 11; Indels 0; Gaps 0;			
Qy	1	DIQWTQSPSSLSASVGRDVITTCASODISNLYNWYQQKPKGAPKLIFYYSSNLHSGVPS	60
Db	1	DIQWTQSPSSLSASVGRDVITTCRASQSISYLSWYQQKFGAPQVLIIYAASLIPSGVPS	60
Qy	61	RFSGGSGTDYTLTISSQLQPEDFATYICYHQYSKLPWTFGGGTKEIKR	108



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:10 ; Search time 175.288 Seconds  
(without alignments)  
1284.140 Million cell updates/sec

Title: US-10-089-500-53

Perfect score: 3071

Sequence: 1 EVQLVSGGDFVPGGSLRV.....IVEFLNRWTFQCSIISTLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq\_16Dec04:\*

1: Geneseqp1990s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3071	100.0	582	4	AAB81987
2	3026	98.5	582	4	AAB81991
3	2780.5	90.5	583	4	AAB83156
4	2760.5	89.9	581	4	AAB81972
5	2750.5	89.6	579	6	AAB83444
6	2750.5	89.6	579	6	AAO30910
7	2719.5	88.6	575	8	ADP42961
8	2621	85.3	580	6	AAO30915
9	2589	84.3	580	6	AAO30913
10	2247	73.2	449	8	ADR23346
11	2246.5	73.2	447	6	AAE33522
12	2240.5	73.0	447	6	AAE33523
13	2238.5	72.9	449	5	AAO18400
14	2238.5	72.9	697	8	ADQ07403
15	2238.5	72.9	697	8	ADQ12180
16	2238.5	72.9	701	8	ADQ07409
17	2238.5	72.9	701	8	ADQ12186
18	2236.5	72.8	447	6	AAE33524
19	2236.5	72.8	450	8	ADH34587
20	2234.5	72.8	445	6	AAO31101
21	2233	72.7	449	6	ABP58273
22	2233	72.7	468	6	ABP58275
23	2232	72.7	451	8	ADH34584
24	2231.5	72.7	444	6	AAE35327
25	2231.5	72.7	444	6	AAE34876

99 2167 70.6 451 2 AAW95661 Mus muscu  
100 2167 70.6 451 3 AAY85201 Light cha

ALIGNMENTS

RESULT 1  
AAB81987  
ID AAB81987 standard; protein; 582 AA.  
XX  
AC AAB81987;  
XX  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.  
XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX  
OS Synthetic.  
XX  
PN WO200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
XX  
PR 30-SEP-1999; 99JP-00278291.  
PR 06-APR-2000; 2000JP-00105088.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
PI WPI; 2001-266143/27.  
XX  
PT New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX  
PS Claim 41; Page 168-172; 183pp; Japanese.  
XX  
CC The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumors, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX  
SQ Sequence 582 AA;  
Query Match 100.0%; Score 3071; DB 4; Length 582;  
Best Local Similarity 100.0%; Pred. No. 2.3e-153;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EVQLVESGGDFVQPGGSLRVSCAAGFAPSHVAMSWVRQAPGKGLEWVAYISSGGSGTY 60  
DB 1 EVQLVESGGDFVQPGGSLRVSCAAGFAPSHVAMSWVRQAPGKGLEWVAYISSGGSGTY 60  
QY 61 SDSVKGRFTISRDNKNTLYLQWRSILRAEDSAVYFCTRVKLGTYFDSWGQGLTLTVSSA 120  
DB 61 SDSVKGRFTISRDNKNTLYLQWRSILRAEDSAVYFCTRVKLGTYFDSWGQGLTLTVSSA 120  
QY 121 STKGSPVFPPLAPSSKTSSTGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSG 180  
DB 121 STKGSPVFPPLAPSSKTSSTGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSG 180  
QY 181 LYSLSVTVTPSSSLGTQTYICNVNHPKSNKTVKDKVEPKSCDKTHTCPPCPAPÉLGGP 240  
DB 181 LYSLSVTVTPSSSLGTQTYICNVNHPKSNKTVKDKVEPKSCDKTHTCPPCPAPÉLGGP 240  
QY 241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300

DB 241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300  
QY 301 TYRVSVLTVLHODWLNQKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360  
DB 301 TYRVSVLTVLHODWLNQKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360  
QY 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKTVDKSRWQ 420  
DB 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKTVDKSRWQ 420  
QY 421 QGNVFSCSVMEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLDLQMLNGINNY 480  
DB 421 QGNVFSCSVMEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLDLQMLNGINNY 480  
QY 481 KNPKLTRMLTFKFMYPKKAATELKHQCLEEBELKPLEEVLNLAQSNFHLRPRDLISNINV 540  
DB 481 KNPKLTRMLTFKFMYPKKAATELKHQCLEEBELKPLEEVLNLAQSNFHLRPRDLISNINV 540  
QY 541 IVLELKGSETTFMCEYADETATIVFEFLNRWITFCQSIISTLT 582  
DB 541 IVLELKGSETTFMCEYADETATIVFEFLNRWITFCQSIISTLT 582

RESULT 2  
AAB81991  
ID AAB81991 standard; protein; 582 AA.  
XX  
AC AAB81991;  
XX  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.  
XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX  
OS Synthetic.  
XX  
PN WO200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
XX  
PR 30-SEP-1999; 99JP-00278291.  
PR 06-APR-2000; 2000JP-00105088.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
PI WPI; 2001-266143/27.  
XX  
PT New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX  
PS Claim 39; Page 175-179; 183pp; Japanese.  
XX  
CC The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumors, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX  
SQ Sequence 582 AA;

Query Match 98.5%; Score 3026; DB 4; Length 582;  
Best Local Similarity 98.3%; Pred. No. 5.2e-151;  
Matches 572; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFASHYAMSVWRQAPKGLEWVAYISSGGSTYY 60  
Db 1 EVTLVESGGDFVQPGGSLKVSCAASGFAFASHYAMSVWRQTPAKRLEWVAYISSGGSTYY 60  
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRVKLGTYYPDSWQGGTLLTVSSA 120  
Db 61 SDSVKGRFTISRDNKNTLYLQWRSLRSEDASMTFCTRVKLGTYYPDSWQGGTLLTVSSA 120  
QY 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVLDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 180  
Db 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVLDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 180  
QY 181 LYSLSVSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELLGGP 240  
Db 181 LYSLSVSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELLGGP 240  
QY 241 SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREBOYNS 300  
Db 241 SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREBOYNS 300  
QY 301 TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDEL 360  
Db 301 TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDEL 360  
QY 361 TKQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRWQ 420  
Db 361 TKQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRWQ 420  
QY 421 QGNVFCSCVMHEALHNHYTKSLSPGKAPTSSSTKTKTQLQLEHLLLDLQMLINGINNY 480  
Db 421 QGNVFCSCVMHEALHNHYTKSLSPGKAPTSSSTKTKTQLQLEHLLLDLQMLINGINNY 480  
QY 481 KNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVNLAQSKNPHLRPRDLISNINV 540  
Db 481 KNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVNLAQSKNPHLRPRDLISNINV 540  
QY 541 IVLELKGSETTFMCEYADETATVFEFLNRWITFCQSIISTLT 582  
Db 541 IVLELKGSETTFMCEYADETATVFEFLNRWITFCQSIISTLT 582

RESULT 3

AAB83156  
ID AAB83156 standard; protein; 583 AA.  
XX AAB83156;  
XX AAB83156;  
DT 02-JUL-2001 (first entry)  
XX Ganglioside GM2 antibody-related protein #1.  
XX Ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer.  
OS Unidentified.

PN WO200123431-A1.  
XX 05-APR-2001.  
XX 29-SEP-2000; 2000WO-JP006775.  
XX 30-SEP-1999; 99JP-00278292.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX Hanai N, Nakamura K, Niwa R;  
XX WPI; 2001-266142/27.  
XX Monoclonal antibodies against ganglioside GM2 combined with drugs,  
PT radioisotopes or proteins for treatment and diagnosis of cancer.  
XX Claim 43; Page 61-65; 80pp; Japanese.

XX  
CC  
CC  
CC  
CC  
XX  
SQ

The present invention relates to derivatives of an antibody against  
ganglioside GM2. The antibody may be a monoclonal antibody or its  
fragments. The antibody is combined with a radioactive isotope, protein  
or small drug in the treatment and diagnosis of cancer

Sequence 583 AA;

Query Match 90.5%; Score 2780.5; DB 4; Length 583;  
Best Local Similarity 89.9%; Pred. No. 41e-138;  
Matches 526; Conservative 22; Mismatches 32; Indels 5; Gaps 2;

QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFASHYAMSVWRQAPKGLEWVAYISSGGSTYY 60  
Db 1 EVQLVQSGAEVKPGASVKSCASGYTFTDYNMDWVKQSPQGLEWGMGYIYPNNGGTGY 60  
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRVKLGTY---PDSWQGGTLLTV 117  
Db 61 NQKPKSKVTITVDTSTSTAYMELHSRSEDATVYYC--ATYGHYYGYMFAYWQGGTLTV 118  
QY 118 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVLDYFPEPTVTSWNSGALTSGVHTFPAVLQ 177  
Db 119 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVLDYFPEPTVTSWNSGALTSGVHTFPAVLQ 178  
QY 178 SGLYSLSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELL 237  
Db 179 SGLYSLSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELL 238  
QY 238 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 297  
Db 239 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 298  
QY 298 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 357  
Db 299 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 358  
QY 358 DELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKS 417  
Db 359 DELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKS 418  
QY 418 RWOQGNVFCSCVMHEALHNHYTKSLSPGKAPTSSSTKTKTQLQLEHLLLDLQMLINGI 477  
Db 419 RWOQGNVFCSCVMHEALHNHYTKSLSPGKAPTSSSTKTKTQLQLEHLLLDLQMLINGI 478  
QY 478 NNYKNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVNLAQSKNPHLRPRDLISN 537  
Db 479 NNYKNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVNLAQSKNPHLRPRDLISN 538  
QY 538 INVIVLELKGSETTFMCEYADETATVFEFLNRWITFCQSIISTLT 582  
Db 539 INVIVLELKGSETTFMCEYADETATVFEFLNRWITFCQSIISTLT 583

RESULT 4

AAB81972  
ID AAB81972 standard; protein; 581 AA.  
XX AAB81972;  
XX AAB81972;  
DT 03-JUL-2001 (first entry)  
XX Ganglioside GD2 specific antibody related protein SEQ ID NO: 31.  
DE Ganglioside; GD2; complementation determining region; CDR; antibody;  
KW mouse; cancer.  
XX Synthetic.  
OS WO200123573-A1.  
PN 05-APR-2001.  
XX 29-SEP-2000; 2000WO-JP006773.  
PF



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XX 30-SEP-1999; 99JP-00278290.
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Hansi N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266163/27.
XX Human type complementation-determining domain transplanted antibody and
PT derivatives against ganglioside GD2, useful in diagnosis and therapy of
PT e.g. tumors, has low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX Example 3; Page 111-114; 123pp; Japanese.
XX
XX The present invention describes an antibody, which can react specifically
CC with ganglioside GD2, and is transplanted with a human type
CC complementation-determining domain (CDR), or its fragments. The antibody
CC and its derivatives are useful in diagnosis and therapy of tumours,
CC particularly cancer diagnosis. The present sequence is a protein used in
CC the exemplification of the invention
XX
XX Sequence 581 AA;
XX
Query Match 89.9%; Score 2760.5; DB 4; Length 581;
Best Local Similarity 90.0%; Pred. No. 4.6e-137;
Matches 524; Conservative 22; Mismatches 35; Indels 1; Gaps 1;
QY 1 EVQLVESGGDFVQPGGSLRVSCAAGSFAPSHVAMSVROAPGKGLEWVAYISSGGSGTY 60
Db 1 QVQLVDSGGLVQPSQTLITCTVSGFSLASTNIHWVQPPGKGLWGLVWAGGS-TNY 59
QY 61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGLTLTVSSA 120
Db 60 NSALMSRLTISKDNKSNQVFLKMSLTAAATAVYCAKESDDYSFAYWGQGLTLTVSSA 119
QY 121 STKGSPVFLPSSKSTSGTAAALGCLVKDYPPPEPTVSVNSGALTSGVHTEPAVLQSG 180
Db 120 STKGSPVFLPSSKSTSGTAAALGCLVKDYPPPEPTVSVNSGALTSGVHTEPAVLQSG 179
QY 181 LYSLSVTVTPSSSLGTQYIICNVNHPKNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGP 240
Db 180 LYSLSVTVTPSSSLGTQYIICNVNHPKNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGP 239
QY 241 SVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
Db 240 SVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299
QY 301 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360
Db 300 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 359
QY 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ 420
Db 360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ 419
QY 421 QGNVFSCSVMEALHNHYTQKSLSLSPGKAPTSSTTKTQLEHLLDQLMILANGINNY 480
Db 420 QGNVFSCSVMEALHNHYTQKSLSLSPGKAPTSSTTKTQLEHLLDQLMILANGINNY 479
QY 481 KNPKLTRMLTFFKYPKPKATLKHQCLBEELKPLEEVNLAKSNFHLRPRDLISNIV 540
Db 480 KNPKLTRMLTFFKYPKPKATLKHQCLBEELKPLEEVNLAKSNFHLRPRDLISNIV 539
QY 541 IVLELKGSETTFMCEVADTATIVFELNRIWITFCOSIISTLT 582
Db 540 IVLELKGSETTFMCEVADTATIVFELNRIWITFCOSIISTLT 581
```

RESULT 5  
AAE33444

ID AAE33444 standard; protein; 579 AA.

```
XX AAE33444;
XX 02-APR-2003 (first entry)
XX
XX KS antibody heavy chain-interleukin 2 (IL-2) fusion protein.
XX Immunoglobulin; diagnosis; epithelial cell adhesion molecule; EPCAM;
KW cancer; gene therapy; interleukin-2; IL2; fusion protein.
XX
XX Unidentified.
XX WO200290566-A2.
XX
XX 14-NOV-2002.
XX
XX 03-MAY-2002; 2002WO-US013844.
XX
XX 03-MAY-2001; 2001US-0288564P.
XX (LEXI-) LEXIGEN PHARM CORP.
XX
XX Gillies SD, Lo K, Qian X;
XX WPI; 2003-111985/10.
XX N-PSDB; AAD51139.
XX
XX New recombinant anti-EpCAM antibody having an amino acid sequence
PT defining an immunoglobulin light or heavy chain framework region, useful
PT for the diagnosis, prognosis and treatment of cancer.
XX
XX Disclosure; Page 80-82; 82pp; English.
XX
XX The present invention relates to novel recombinant anti-EpCAM (human
CC epithelial cell adhesion molecule) antibodies comprising an amino acid
CC sequence defining an immunoglobulin light or heavy chain framework
CC region. Sequences of the present invention are useful for the diagnosis,
CC prognosis and treatment of cancer. They are also used in gene therapy.
CC The present sequence is KS antibody heavy chain-interleukin 2 (IL-2)
CC fusion protein. This sequence is used to illustrate the method of the
CC invention
XX
XX Sequence 579 AA;
Query Match 89.6%; Score 2750.5; DB 6; Length 579;
Best Local Similarity 88.5%; Pred. No. 1.5e-136;
Matches 516; Conservative 32; Mismatches 30; Indels 5; Gaps 2;
QY 1 EVQLVESGGDFVQPGGSLRVSCAAGSFAPSHVAMSVROAPGKGLEWVAYISSGGSGTY 60
Db 1 QIQLVDSGAEVKKPGETVKISKASGYFTFYGMWVVKQTFCGLKMWGWINTYTGEPTY 60
QY 61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTR-VKLGTYYFDSWGQGLTLTVSS 119
Db 61 ADPPKGRFAPLSLETSTSTAFILQINLRSEDTATYFCVRFISKGDY---WGQGSTVTVSS 116
QY 120 ASTKGSPVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVSVNSGALTSGVHTEPAVLQSS 179
Db 117 ASTKGSPVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVSVNSGALTSGVHTEPAVLQSS 176
QY 180 GLYSLSVTVTPSSSLGTQYIICNVNHPKNTKVDKKVEPKSCDKTHTCPPCPAPPELLGG 239
Db 177 GLYSLSVTVTPSSSLGTQYIICNVNHPKNTKVDKRVPEKSCDKTHTCPPCPAPPELLGG 236
QY 240 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
Db 237 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 296
QY 300 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 359
Db 297 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 356
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 419
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Db 357 MTKNQVSLTCLVGFYPSDIAVWESNGQENNYKTPPVLDSDGSFLLYKLTVDKSRW 416  
Qy 420 QQGVNFSCVWHEALHNHYTKSLSPGKAPTSSSTKKTQLOLEHLLDQLMILNGINN 479  
Db 417 QQGVNFSCVWHEALHNHYTKSLSPGKAPTSSSTKKTQLOLEHLLDQLMILNGINN 476  
Qy 480 YKNPKLTRMLTFKPYMPKKATELKHLCLEEBELKPLEEVLNLAQSKNFHLRPRDLISIN 539  
Db 477 YKNPKLTRMLTFKPYMPKKATELKHLCLEEBELKPLEEVLNLAQSKNFHLRPRDLISIN 536  
Qy 540 VIVLELKGSETTFMCEYADETATVEFLNRWITFCOSIISTLT 582  
Db 537 VIVLELKGSETTFMCEYADETATVEFLNRWITFCOSIISTLT 579

RESULT 6  
AAO30910  
ID AAO30910 standard; protein; 579 AA.  
XX AC AAO30910;  
XX AC  
DT 22-SEP-2003 (first entry)  
XX di-KS-ala-IL2 (D20T) variant protein.  
DE Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;  
KW gene therapy; immunoglobulin; Ig; fusion protein; human.  
XX Homo sapiens.  
OS Unidentified.  
OS Chimeric.  
XX WO2003048334-A2.  
XX 12-JUN-2003.  
XX 04-DEC-2002; 2002WO-US038780.  
XX 04-DEC-2001; 2001US-0337113P.  
PR 12-APR-2002; 2002US-0371966P.  
XX (EMDL-) EMD LEXIGEN RES CENT CORP.  
PA Gillies SD;  
XX WPI; 2003-513757/48.  
XX New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2  
PT moiety, useful for preparing a composition for treating cancer, viral  
PT infections or immune disorders.  
XX Example 10; Page 60-63; 71pp; English.  
XX The invention relates to cytokine fusion proteins with increased  
CC therapeutic index and methods for increasing the therapeutic index of  
CC such fusion proteins. The fusion protein comprises a non-interleukin-2  
CC (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a  
CC composition for treating cancer, viral infections or immune disorders.  
CC The fusion protein is also used in gene therapy. The present sequence is  
CC di-KS-ala-IL2 (D20T) variant protein comprising di-KS heavy chain fused  
CC to human IL-2 (D20T) variant protein. This sequence is used to illustrate  
CC the method of the invention  
XX Sequence 579 AA;  
Query Match 89.6%; Score 2750.5; DB 6; Length 579;  
Best Local Similarity 88.5%; Pred. No. 1.5e-136;  
Matches 516; Conservative 32; Mismatches 30; Indels 5; Gaps 2;  
Qy 1 EVOLVESGGDFVDPGGSLRVSCAAGFAPSHYAMSWRQAPGKLEWYVYISSGGSGTY 60  
Db 1 QIQLVQSGPELKKPGSSVKISKASGYTFTNYGMNVRQAPGKGLKWMGMINITYTGEPT 60

Qy 61 SDSVKGRFTISRDNSTLYLQMRSLRAEDSAVYFCTR-VKLGTYYPDSWGQGTLLTVSS 119  
Db 61 ADDFKGRFTIARTSTSLYLQNLRLSEDATYFCVRPISKGDY----WGQGTTLTVSS 116  
Qy 120 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYPPPEPTVTSWNSGALTSGVHTTTPAVLQSS 179  
Db 117 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYPPPEPTVTSWNSGALTSGVHTTTPAVLQSS 176  
Qy 180 GLYSLSVVTVPSSSISLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPPCPAPELGG 239  
Db 177 GLYSLSVVTVPSSSISLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPPCPAPELGG 236  
Qy 240 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPRBEQYN 299  
Db 237 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPRBEQYN 296  
Qy 300 STYRVSVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 359  
Db 297 STYRVSVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 356  
Qy 360 LTKNQVSLTCLVKGFYPSDIAVWESNGQENNYKTPPVLDSDGSFLLYKLTVDKSRW 419  
Db 357 MTKNQVSLTCLVKGFYPSDIAVWESNGQENNYKTPPVLDSDGSFLLYKLTVDKSRW 416  
Qy 420 QQGVNFSCVWHEALHNHYTKSLSPGKAPTSSSTKKTQLOLEHLLDQLMILNGINN 479  
Db 417 QQGVNFSCVWHEALHNHYTKSATATPCGAPTSSSTKKTQLOLEHLLDQLMILNGINN 476  
Qy 480 YKNPKLTRMLTFKPYMPKKATELKHLCLEEBELKPLEEVLNLAQSKNFHLRPRDLISIN 539  
Db 477 YKNPKLTRMLTFKPYMPKKATELKHLCLEEBELKPLEEVLNLAQSKNFHLRPRDLISIN 536  
Qy 540 VIVLELKGSETTFMCEYADETATVEFLNRWITFCOSIISTLT 582  
Db 537 VIVLELKGSETTFMCEYADETATVEFLNRWITFCOSIISTLT 579

RESULT 7  
ADP42961  
ID ADP42961 standard; protein; 575 AA.  
XX ADP42961;  
XX AC  
DT 23-SEP-2004 (first entry)  
XX Humanised immunoglobulin heavy chain-IL-2 fusion protein SEQ ID NO:6.  
DE immunoglobulin; variable region; antibody; GD2; cytostatic; gene therapy;  
KW cancer; cell surface glycosphingolipid; IL-2.  
XX Synthetic.  
XX WO2004055056-A1.  
PN 01-JUL-2004.  
XX 16-DEC-2003; 2003WO-EP014295.  
XX 17-DEC-2002; 2002US-0433945P.  
PR (MERE ) MERCK PATENT GMBH.  
XX Gillies SD, Lo K;  
XX WPI; 2004-488049/46.  
DR N-PSDB; ADP42959.  
XX New modified m14.18 antibodies with reduced immunogenicity and that  
PT specifically bind the human cell surface glycosphingolipid GD2, useful  
PT for treating cancer.  
XX Disclosure; SEQ ID NO 6; 51pp; English.  
PS



Qy	540	VIVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISTLT	582
Db	538	VIVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISTLT	580
RESULT 9			
AAO30913			
ID	AAO30913	standard; protein; 580 AA.	
AC	AAO30913;		
DT	22-SEP-2003	(first entry)	
DE	di-NHS76 (gamma2h) (FN-AQ)-ala-IL2 (D20T) variant protein.		
KW	Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;		
KW	gene therapy; immunoglobulin; Ig; fusion protein; human; variant.		
OS	Homo sapiens.		
OS	Unidentified.		
OS	Chimeric.		
PN	WO2003048334-A2.		
PD	12-JUN-2003.		
PF	04-DEC-2002; 2002WO-US038780.		
PR	04-DEC-2001; 2001US-0337113P.		
PR	12-APR-2002; 2002US-0371966P.		
XX	(EMDL-) EMD LEXIGEN RES CENT CORP.		
XX	Gillies SD;		
XX	WPI; 2003-513757/48.		
PT	New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2		
PT	moiety, useful for preparing a composition for treating cancer, viral		
PT	infections or immune disorders.		
XX	Claim 37; Page 64-67; 71pp; English.		
CC	The invention relates to cytokine fusion proteins with increased		
CC	therapeutic index and methods for increasing the therapeutic index of		
CC	such fusion proteins. The fusion protein comprises a non-interleukin-2		
CC	(IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a		
CC	composition for treating cancer, viral infections or immune disorders.		
CC	The fusion protein is also used in gene therapy. The present sequence is		
CC	di-NHS76 (gamma2h) (FN-AQ)-ala-IL2 (D20T) variant protein comprising di-		
CC	KS heavy chain fused to human IL-2 (D20T) variant protein. This sequence		
CC	is used to illustrate the method of the invention		
XX	Sequence 580 AA;		
Query Match			
Best Local Similarity 84.3%; Score 2589; DB 6; Length 580;			
Matches 497; Conservative 29; Mismatches 52; Indels 6; Gaps 5;			
Qy	1	EVQLVESGGDFVPGGSLRVSRAASGPAFSGH-YAMSWVRQAPGKLEWVAYISGGSGTY 59	
Db	1	QVQLQESGGPLVKPSETLSLTCAVSGYSISSGYWGIQPPGKLEWIGSIYHSGS-TY 59	
Qy	60	YSDSVKGRFTISRDNKNTLYLQWRSRAEDSAVYFCTRVLKLTGYTDSGQGTLLTVSS 119	
Db	60	YNPSLKRVTISVDTSKNQFSLKLSVTAADATVYVCARGKWSK--FDYWGQGTLLTVSS 117	
Qy	120	-ASTKGPSVPLAPSSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS 178	
Db	118	GASTKGPSVPLAPCSKSTSESTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS 177	
Qy	179	SGLYSLSVVTVFPSSSLGTQTYICNVNHPKPSNTKVDKVPKSCDKTHTCPPCPAPELLG 238	
Db	178	SGLYSLSVVTVFPSSNFGTQTYTCNVNHPKPSNTKVDKVPKSCDKTHTCPPCPAPP-VA 236	
Qy	239	GPSVELFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 298	
Db	237	GPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQA 296	
Qy	299	NSTYRVVSVLTVHLQDMLNGKYKCKVSNNKALPAPIEKTIISKAKGQPREPQVYTLPPSRD 358	
Db	297	QSTFRVSVVLTVVHQDMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSR 356	
Qy	359	ELTNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLSDDSGSFYLSKLTVDKSR 418	
Db	357	EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPMLDSGDSFFLYSKLTVDKSR 416	
Qy	419	WQGNVFCSCVMEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLDLQMLNGIN 478	
Db	417	WQGNVFCSCVMEALHNHYTQKSATATPGAAATSSSTKKTQLQLEHLLDLQMLNGIN 476	
Qy	479	NYKNPKLTRMLTFKYPMPKKATELKHLQCLEELKPLEEVNLNLAQSKNFHLRPDLISNI 538	
Db	477	NYKNPKLTRMLTFKYPMPKKATELKHLQCLEELKPLEEVNLNLAQSKNFHLRPDLISNI 536	
Qy	539	NVIVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISTLT	582
Db	537	NVIVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISTLT	580
RESULT 10			
ADR23346			
ID	ADR23346	standard; protein; 449 AA.	
XX	ADR23346;		
DT	04-NOV-2004	(first entry)	
DE	Human CD72-targeted IgG1 heavy chain.		
KW	Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;		
KW	immunosuppressive; cancer; autoimmune disease; gene therapy.		
OS	Homo sapiens.		
Key	Location/Qualifiers		
Region	1..119	/label= V_region	
Region	120..449	/label= C_region	
XX	WO2004067569-A1.		
PD	12-AUG-2004.		
XX	27-JAN-2003; 2003WO-EP050004.		
XX	27-JAN-2003; 2003WO-EP050004.		
XX	(CRUC-) CRUCCELL HOLLAND BV.		
XX	Bakker ABH, Marissen WE;		
DR	WPI; 2004-580978/56.		
DR	N-PSDB; ADR23345.		
XX	New internalizing human binding molecules capable of specifically binding		
PT	to CD72, useful for diagnosing and/or treating B-cell associated		
PT	diseases, such as cancer or autoimmune disorders.		
XX	Claim 69; SEQ ID NO 38; 174pp; English.		
XX	The present sequence is the protein sequence of the heavy chain of human		
CC	IgG1 antibody 004, which specifically recognises human B cell associated		
CC	antigen CD72. An scFv ADR23320 selected from an antibody phage display		

CC library was shown to specifically recognise the human CD72 receptor. The  
 CC scFv was recloned in IGG expression vector C01 using primers designed to  
 CC restore complete human frameworks, thereby generating antibody 004. Such  
 CC anti-CD72 immunoglobulins or their antigen-binding fragments can be used  
 CC as internalising human binding molecules of the invention. These  
 CC internalising human binding molecules are capable of (specifically)  
 CC binding to CD72 or its antigenic determinant, and preferably bind to CD72  
 CC associated with cells. Upon binding to CD72 present on the surface of  
 CC target cells, the binding molecules internalise. In addition to the  
 CC internalising human binding molecules, the invention provides  
 CC immunconjugates comprising an internalising human binding molecule and a  
 CC tag (toxic substance, radioactive substance, liposome and/or enzyme),  
 CC nucleic acids encoding these, and compositions comprising them. The  
 CC internalising human binding molecule, immunconjugate, nucleic acid  
 CC molecule or composition can be used in the diagnosis and/or treatment of  
 CC a B cell associated disorder or disease, especially a B cell associated  
 CC cancer and B cell associated autoimmune disorder (claimed). An  
 CC internalising human binding molecule comprising the present heavy chain  
 CC sequence is specifically claimed.  
 XX  
 SQ Sequence 449 AA;

Query Match 73.2%; Score 2247; DB 8; Length 449;  
 Best Local Similarity 94.0%; Pred. No. 3.3e-110;  
 Matches 422; Conservative 9; Mismatches 18; Indels 0; Gaps 0;  
 QY 1 EVQLVESGDFVQPGSLRVCAASGFAPSHVAMSWVRQAPGKLEWVAIYSGSGGTYY 60  
 DB tag (toxic substance, radioactive substance, liposome and/or enzyme),  
 1 EVQLVESGGLVQPGSLRVCAASGFTFGLMSVWRQAPGKLEWVAIYSGSNKYY 60  
 QY 61 SDSVKGRFTISRDNSKNTLYLQMSLRADSAVYFCTRVKLGTYYFDWSGQGTLLTVSSA 120  
 DB 61 ADSVKGRFTISRDNSKNTLYLQMSLRADSAVYFCTRVKLGTYYFDWSGQGTLLTVSSA 120  
 QY 121 STKGPSVFPFLAPSSKTSSTGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSG 180  
 DB 121 STKGPSVFPFLAPSSKTSSTGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSG 180  
 QY 181 LYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDRKVEPKSCDKTHCTCPPELGGP 240  
 DB 181 LYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDRKVEPKSCDKTHCTCPPELGGP 240  
 QY 241 SVFLPPPKDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNNAKTKPREQYNS 300  
 DB 241 SVFLPPPKDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNNAKTKPREQYNS 300  
 QY 301 TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360  
 DB 301 TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360  
 QY 361 TKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ 420  
 DB 361 TKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ 420  
 QY 421 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449  
 DB 421 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449

RESULT 11  
 AAE33522  
 ID AAE33522 standard; protein; 447 AA.  
 XX  
 AC AAE33522;  
 XX  
 DT 02-APR-2003 (first entry)  
 XX Human AQC2 heavy chain protein.  
 XX Human; very late activation antigen; VLA-1; betal containing integrin;  
 KW immunological disorder; inflammatory disorder; skin related condition;  
 KW psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;  
 KW fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;

fever; migraine headache; inflammatory bowel disease; Crohn's disease;  
 irritable bowel syndrome; colitis; colorectal cancer; vascular disease;  
 atherosclerosis; thyroiditis; aplastic anaemia; periarteritis nodosa;  
 gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;  
 osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;  
 systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;  
 renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;  
 hypersensitivity; graft rejection; transplant rejection; conjunctivitis;  
 graft versus host disease; myocardial ischaemia.  
 Homo sapiens.  
 WO200283854-A2.  
 24-OCT-2002.  
 12-APR-2002; 2002WO-US011521.  
 13-APR-2001; 2001US-0283794P.  
 06-JUL-2001; 2001US-0303689P.  
 (BIOJ ) BIOGEN INC.  
 Lyne PD, Garber EA, Saldanha JW, Karpusas M;  
 WPI; 2003-093009/08.  
 New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-  
 mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,  
 burns, dermatitis, and abnormal proliferation of hair follicle cells or  
 fibrosis.  
 Claim 6; Page 75; 248pp; English.

The present invention relates to novel antibodies that specifically bind  
 to very late activation (VLA-1; betal containing integrins) antigens and  
 methods of using these antibodies to treat immunological disorders. The  
 anti-VLA-1 antibodies are useful for preventing or treating VLA-1-  
 mediated immunological or inflammatory disorders such as skin related  
 conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal  
 proliferation of hair follicle cells), fibrosis (e.g. kidney or lung  
 fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,  
 bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-  
 intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,  
 gastritis, irritable bowel syndrome, colitis and colorectal cancer),  
 vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,  
 periarthritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,  
 autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid  
 arthritis, systemic lupus erythematosus and multiple sclerosis), renal  
 failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,  
 polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or  
 immediate hypersensitivity), graft and transplant rejections, graft  
 versus host disease, conjunctivitis, swelling occurring after injury, is  
 myocardial ischaemia or endotoxin shock syndrome. The present sequence is  
 human AQC2 heavy chain protein

Sequence 447 AA;  
 Query Match 73.2%; Score 2246.5; DB 6; Length 447;  
 Best Local Similarity 95.1%; Pred. No. 3.5e-110;  
 Matches 426; Conservative 4; Mismatches 17; Indels 1; Gaps 1;  
 QY 1 EVQLVESGDFVQPGSLRVCAASGFAPSHVAMSWVRQAPGKLEWVAIYSGSGGTYY 60  
 DB 1 EVQLVESGGLVQPGSLRVCAASGFTFRTYMSVWRQAPGKLEWVAIYSGGH-TYY 59  
 QY 61 SDSVKGRFTISRDNSKNTLYLQMSLRADSAVYFCTRVKLGTYYFDWSGQGTLLTVSSA 120  
 DB 60 LDSVKGRFTISRDNSKNTLYLQMSLRADSAVYFCTRVKLGTYYFDWSGQGTLLTVSSA 119  
 QY 121 STKGPSVFPFLAPSSKTSSTGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSG 180  
 DB 120 STKGPSVFPFLAPSSKTSSTGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSG 179

QY 181 LYSLSVVTVTPSSSLGTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPPELLGGP 240  
 |||||  
 DB 180 LYSLSVVTVTPSSSLGTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPPELLGGP 239  
 |||||  
 QY 241 SVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREEQYNS 300  
 |||||  
 DB 240 SVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREEQYNS 299  
 |||||  
 QY 301 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360  
 |||||  
 DB 300 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359  
 |||||  
 QY 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLKLTVDKSRWQ 420  
 |||||  
 DB 360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLKLTVDKSRWQ 419  
 |||||  
 QY 421 QGNVFSCSVNHEALHNHYTQKSLSLSPG 448  
 |||||  
 DB 420 QGNVFSCSVNHEALHNHYTQKSLSLSPG 447  
 |||||

RESULT 12  
 AAE33523  
 ID AAE33523 standard; protein; 447 AA.  
 XX  
 AC AAE33523;  
 XX  
 DT 02-APR-2003 (first entry)  
 XX  
 DE Human AQC2 heavy chain mutant protein, haaQC2.  
 XX  
 KW Human; very late activation antigen; VLA-1; betal containing integrin;  
 KW immunological disorder; inflammatory disorder; skin related condition;  
 KW psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;  
 KW fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;  
 KW fever; migraine headache; inflammatory bowel disease; Crohn's disease;  
 KW irritable bowel syndrome; colitis; colorectal cancer; vascular disease;  
 KW atherosclerosis; thyroiditis; aplastic anaemia; periarthritis nodosa;  
 KW gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;  
 KW osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;  
 KW systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;  
 KW renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;  
 KW hypersensitivity; graft rejection; transplant rejection; conjunctivitis;  
 KW graft versus host disease; myocardial ischaemia; mutant; mutein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283854-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 12-APR-2002; 2002WO-US011521.  
 XX  
 PR 13-APR-2001; 2001US-0283794P.  
 PR 06-JUL-2001; 2001US-0303689P.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 XX  
 PI Lyne PD, Garber EA, Saldanha JW, Karpueas M;  
 XX  
 DR WPI; 2003-093009/08.  
 XX  
 PT New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-  
 PT mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,  
 PT burns, dermatitis, and abnormal proliferation of hair follicle cells or  
 PT fibrosis.  
 XX  
 PS Example 23; Page 91-92; 248pp; English.  
 XX  
 CC The present invention relates to novel antibodies that specifically bind  
 CC to very late activation (VLA-1; betal containing integrins) antigens and  
 CC methods of using these antibodies to treat immunological disorders. The

CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-  
 CC mediated immunological or inflammatory disorders such as skin related  
 CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal  
 CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung  
 CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,  
 CC bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-  
 CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,  
 CC gastritis, irritable bowel syndrome, colitis and colorectal cancer),  
 CC psoriasis, atherosclerosis, thyroiditis, aplastic anaemia,  
 CC parietaritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,  
 CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid  
 CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal  
 CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,  
 CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or  
 CC immediate hypersensitivity), graft and transplant rejections, graft  
 CC versus host disease, conjunctivitis, swelling occurring after injury,  
 CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is  
 CC human AQC2 heavy chain mutant protein, haaQC2  
 XX  
 XX Sequence 447 AA;  
 Query Match 73.0%; Score 2240.5; DB 6; Length 447;  
 Best Local Similarity 94.9%; Pred. No. 7.2e-110;  
 Matches 425; Conservative 4; Mismatches 18; Indels 1; Gaps 1;  
 QY 1 EVOLVESGGDFVQPGGSLRVSCAASGFAPFSYAMSVVRQAPGKLEWAVYISGGSGTYY 60  
 |||||  
 DB 1 EVOLVESGGGLVQPGGSLRVSCAASGFTFSRYTMSVVRQAPGKLEWAVYISGGH-TYY 59  
 |||||  
 QY 61 SDSVKGRFTISRDNKNTLYLQWNSLRABDTAVYCTRGDGGYFDVWQGLTVTVSSA 120  
 |||||  
 DB 60 LDSVKGRFTISRDNKNTLYLQWNSLRABDTAVYCTRGDGGYFDVWQGLTVTVSSA 119  
 |||||  
 QY 121 STKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSG 180  
 |||||  
 DB 120 STKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSG 179  
 |||||  
 QY 181 LYSLSVWTVTPSSSLGTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPPELLGGP 240  
 |||||  
 DB 180 LYSLSVWTVTPSSSLGTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPPELLGGP 239  
 |||||  
 QY 241 SVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREEQYNS 300  
 |||||  
 DB 240 SVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREEQYNS 299  
 |||||  
 QY 301 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360  
 |||||  
 DB 300 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359  
 |||||  
 QY 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLKLTVDKSRWQ 420  
 |||||  
 DB 360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLKLTVDKSRWQ 419  
 |||||  
 QY 421 QGNVFSCSVNHEALHNHYTQKSLSLSPG 448  
 |||||  
 DB 420 QGNVFSCSVNHEALHNHYTQKSLSLSPG 447  
 |||||

RESULT 13  
 AAO18400  
 ID AAO18400 standard; protein; 449 AA.  
 XX  
 AC AAO18400;  
 XX  
 DT 11-OCT-2002 (first entry)  
 XX  
 DE Mature humanised murine CBE11 heavy chain variable domain.  
 XX  
 KW Mouse; humanised antibody; lymphotoxin beta receptor; antibody; cancer;  
 KW neoplasia; LT-beta-R; light chain; heavy chain; variable region.  
 XX  
 OS Mus sp.  
 OS Synthetic.

```
XX PN WO200230986-A2.
XX PD 18-APR-2002.
XX XX 12-OCT-2001; 2001WO-US032140.
XX PF 13-OCT-2000; 2000US-0240285P.
XX PR 13-MAR-2001; 2001US-0275289P.
XX PR 21-JUN-2001; 2001US-0299987P.
XX XX (BIOI ) BIOGEN INC.
XX PA Garber E, Lyne P, Saldanha JW;
XX PI WPI; 2002-583337/62.
XX DR New humanized anti-lymphotoxin-beta receptor antibody, useful for
XX PT treating or reducing the advancement, severity or effects of neoplasia,
XX PT particularly solid tumors (i.e. carcinomas) including colorectal cancer
XX PT and breast cancer.
XX PS Example 5; Page 25-26; 41pp; English.
XX CC The present invention relates to humanised anti-lymphotoxin beta receptor
XX CC (LT-beta-R) antibodies. These are derived from the murine LT-beta-R
XX CC binding antibody CBEL1 and can be used to treat neoplasia in humans. The
XX CC present sequence is a humanised murine CBEL1 heavy chain variable region
XX SQ Sequence 449 AA;

Query Match 72.9%; Score 2238.5; DB 5; Length 449;
Best Local Similarity 94.0%; Pred. No. 9.2e-110;
Matches 422; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

QY 1 EVQLVESGGDFVQPGSLRVS CAAGFAPSHYAMSVRQAPGKGLEWVAYISSGSGTY 60
DB 1 EVQLVESGGGLVKPGSLRSLSCAAGFTFSDYMWFRQAPGKGLEWATISDGGSYTY 60
QY 61 SDSVKGRTISRDNKNTLYLQMSLRADSAVYFCTRVKLTGTYFDSWGGGTLTVSS 119
DB 61 PDSVKGRTISRDNKNTLYLQMSLRADSAVYFCTRVKLTGTYFDSWGGGTLTVSS 120
QY 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
DB 121 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 180
QY 180 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSN TKVDKVEPKSCDKTHTCPPCPAPELLGG 239
DB 181 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSN TKVDKVEPKSCDKTHTCPPCPAPELLGG 240
QY 240 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNAKTKPREEQYN 299
DB 241 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNAKTKPREEQYN 300
QY 300 STYRVVSVLTVLDHQLWNGKEYCKVSKNKA LPAPEKTIISKAKGPQREPOVYTLPPSRDE 359
DB 301 STYRVVSVLTVLDHQLWNGKEYCKVSKNKA LPAPEKTIISKAKGPQREPOVYTLPPSRDE 360
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 419
DB 361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 420
QY 420 QQGNVFSCVMHEALHNHYTQKSLSLSPG 448
DB 421 QQGNVFSCVMHEALHNHYTQKSLSLSPG 449

RESULT 14
ADQ07403
ID ADQ07403 standard; protein; 697 AA.
XX AC ADQ07403;
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XX DT 07-OCT-2004 (first entry)
XX DE hCBEL1/hBHA10 bispecific-1 antibody construct mature heavy chain.
XX KW tumour volume; lymphotoxin-beta receptor; LT-beta-R; agonist; antibody;
XX KW chemotherapeutic; supra-additive; inhibition; cytostatic; gene therapy;
XX KW cancer; mature heavy chain; hCBEL1/hBHA10 bispecific-1.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2004058183-A2.
XX PD 15-JUL-2004.
XX PF 22-DEC-2003; 2003WO-US041243.
XX PR 20-DEC-2002; 2002US-0435185P.
XX PA (BIOG-) BIOGEN IDEC MA INC.
XX PI Lepage D, Gill A;
XX DR WPI; 2004-525785/50.
XX DR N-PSDB; ADQ07402.
XX PT Inhibiting tumor volume comprising administering an amount of a
XX PT lymphotoxin-beta receptor agonist or antibody and a chemotherapeutic
XX PT agent (e.g. gemcitabine or adriamycin).
XX PS Disclosure; SEQ ID NO 2; 161pp; English.
XX CC The invention relates to a novel method for inhibiting tumour volume. The
XX CC method comprises administering an amount of a lymphotoxin-beta receptor
XX CC (LT-beta-R) agonist or antibody and an amount of at least one
XX CC chemotherapeutic agent, where the administration of the LT-beta-R agonist
XX CC or antibody and the chemotherapeutic agent results in supra-additive
XX CC inhibition of the tumour. The invention further relates to: a
XX CC pharmaceutical composition comprising an amount of an LT-beta-R agonist
XX CC and at least one chemotherapeutic agent, and a pharmaceutical carrier,
XX CC which upon administration to a subject results in supra-additive
XX CC inhibition of a tumour. The lymphotoxin-beta receptor agents have
XX CC cytostatic activity. Gene therapy may be used in the tumour inhibition
XX CC method. The method is useful for inhibiting tumour volume or for treating
XX CC cancer. The lymphotoxin-beta receptor agonist and the chemotherapeutic
XX CC agent are useful for preparing a medicament for the treatment of cancer,
XX CC which upon administration to a subject results in supra-additive
XX CC inhibition of a tumour. This sequence represents the mature heavy chain
XX CC of the hCBEL1/hBHA10 bispecific-1 antibody construct for use in the
XX CC tumour volume inhibition method of the invention.
XX SQ Sequence 697 AA;

Query Match 72.9%; Score 2238.5; DB 8; Length 697;
Best Local Similarity 94.0%; Pred. No. 1.4e-109;
Matches 422; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

QY 1 EVQLVESGGDFVQPGSLRVS CAAGFAPSHYAMSVRQAPGKGLEWVAYISSGSGTY 60
DB 1 EVQLVESGGGLVKPGSLRSLSCAAGFTFSDYMWFRQAPGKGLEWATISDGGSYTY 60
QY 61 SDSVKGRTISRDNKNTLYLQMSLRADSAVYFCTRVKLTGTYFDSWGGGTLTVSS 119
DB 61 PDSVKGRTISRDNKNTLYLQMSLRADSAVYFCTRVKLTGTYFDSWGGGTLTVSS 120
QY 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
DB 121 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 180
QY 180 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSN TKVDKVEPKSCDKTHTCPPCPAPELLGG 239
DB 181 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSN TKVDKVEPKSCDKTHTCPPCPAPELLGG 240
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:59:16 ; Search time 44.1842 Seconds  
(without alignments)  
983.287 Million cell updates/sec

**Title:** US-10-089-500-53

**Perfect score:**

Sequence: 1 EVQLVESGGDFVQPGGSLRV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

**Total number of hits satisfying chosen parameters: 513545**

Minimum DB Req Length: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 02

POST-PROCESSING: MINIMUM MATCH 0%  
MAXIMUM MATCH 100%

Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents 22.\*

Database : Issued Patents AA:\*

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.per:

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3: /cgn2_6/ptodata/1/1aa/6A_COMB.per:

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3: /cgn2_6/ptodata/1/1aa/6A_COMB.per:
4: /cgn2_6/ptodata/1/1aa/6B_COMB.per:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:
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3: /cgn2_6/ptodata/1/iaa/c1003003.p  
6: /cgn2_6/ptodata/1/iaa/backfiles1.pe
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	2194.5	71.5	452	3	US-09-027-449-71	Sequence 71, Appl	
2	2194.5	71.5	452	3	US-09-026-985-71	Sequence 71, Appl	
3	2194.5	71.5	452	4	US-09-121-9528-71	Sequence 71, Appl	
4	2194.5	71.5	452	4	US-09-234-340A-71	Sequence 71, Appl	
5	2194.5	71.5	459	1	US-08-157-101A-7	Sequence 7, Appl	
6	2169	70.6	453	3	US-08-466-151-8	Sequence 8, Appl	
7	2169	70.6	453	3	US-08-466-163B-8	Sequence 8, Appl	
8	2169	70.6	453	3	US-09-802-096-8	Sequence 8, Appl	
9	2169	70.6	453	4	US-08-802-077-8	Sequence 8, Appl	
10	2167	70.6	451	2	US-08-887-352B-14	Sequence 14, Appl	
11	2167	70.6	451	2	US-08-887-352B-16	Sequence 16, Appl	
12	2167	70.6	451	3	US-08-466-151-65	Sequence 65, Appl	
13	2167	70.6	451	3	US-09-109-207C-14	Sequence 14, Appl	
14	2167	70.6	451	3	US-09-109-207C-16	Sequence 16, Appl	
15	2167	70.6	451	3	US-09-296-005-14	Sequence 14, Appl	
16	2167	70.6	451	3	US-09-296-005-16	Sequence 16, Appl	
17	2167	70.6	451	4	US-09-320-171-14	Sequence 14, Appl	
18	2167	70.6	451	4	US-09-320-171-16	Sequence 16, Appl	
19	2167	70.6	451	4	US-09-716-028-14	Sequence 14, Appl	
20	2167	70.6	451	4	US-09-716-028-16	Sequence 16, Appl	
21	2167	70.6	451	4	US-10-113-996-14	Sequence 14, Appl	
22	2167	70.6	451	4	US-10-113-996-16	Sequence 16, Appl	
23	2163	70.4	451	2	US-08-887-352B-18	Sequence 18, Appl	
24	2163	70.4	451	3	US-09-109-207C-18	Sequence 18, Appl	
25	2163	70.4	451	3	US-09-282-505-2	Sequence 2, Appl	
26	2163	70.4	451	3	US-09-054-255-2	Sequence 2, Appl	
27	2163	70.4	451	3	US-09-296-005-18	Sequence 18, Appl	

## ALIGNMENTS

RESULT 1  
US-09-027-449-71  
; Sequence 71, Application US/09027449  
; Patent No. 6025158  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/027,449  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/074,330  
; FILING DATE: 22-Jan-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/038,664  
; FILING DATE: 21-Feb-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R3-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 452 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-09-027-449-71

Query Match 71.5%; Score 2194.5; DB 3; Length 452;  
Best Local Similarity 90.9%; Pred. No. 2.5e-161;  
Matches 411; Conservative 14; Mismatches 24; Indels 3; Gaps 1;  
QY 1 EVOLVESGDFVQPGSLRVSCAASGFASFHYAMSVWRQAPGKGLEWVAYISSGSGTYY 60  
DB 1 EVOLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHVWRQAPGKGLEWVGIDPSNGETTY 60  
QY 61 SDSVKGRTISRDNSTNTLYLQMRSLRAEDSAVYFCTRVKL---GTYYPDSWGQGLTV 117  
DB 61 NQKFKGRFTLSRDNSKNTAYLQNSLRAEDTAVYICARGDYRNGDWFVDMVGGQGLTV 120  
QY 118 SSASTKGPSVFPPLAPSSTSGTAAALGCLVKDYPPEPTVSVNSGALTSGVHTTFAVLQ 177  
DB 121 SSASTKGPSVFPPLAPSSTSGTAAALGCLVKDYPPEPTVSVNSGALTSGVHTTFAVLQ 180  
QY 178 SGLYSLSSVTVTPSSSLGTQYICNVNHPKNTKVDKVPKSCDKTHTCPCPAPELL 237  
DB 181 SGLYSLSSVTVTPSSSLGTQYICNVNHPKNTKVDKVPKSCDKTHTCPCPAPELL 240  
QY 238 GGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297

DB 241 GGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300  
QY 298 YNSTYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 357  
DB 301 YNSTYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 360  
QY 358 DELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSGDSGFFLYSKLTVDKS 417  
DB 361 EEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSGDSGFFLYSKLTVDKS 420  
QY 418 RWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449  
DB 421 RWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452  
RESULT 2  
US-09-026-985-71  
; Sequence 71, Application US/09026985  
; Patent No. 6133426  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/026,985  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R3-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 452 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-09-026-985-71

Query Match 71.5%; Score 2194.5; DB 3; Length 452;  
Best Local Similarity 90.9%; Pred. No. 2.5e-161;  
Matches 411; Conservative 14; Mismatches 24; Indels 3; Gaps 1;  
QY 1 EVOLVESGDFVQPGSLRVSCAASGFASFHYAMSVWRQAPGKGLEWVAYISSGSGTYY 60  
DB 1 EVOLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHVWRQAPGKGLEWVGIDPSNGETTY 60  
QY 61 SDSVKGRTISRDNSTNTLYLQMRSLRAEDSAVYFCTRVKL---GTYYPDSWGQGLTV 117  
DB 61 NQKFKGRFTLSRDNSKNTAYLQNSLRAEDTAVYICARGDYRNGDWFVDMVGGQGLTV 120  
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DB 121 SSASTKGPSVFPPLAPSSTSGTAAALGCLVKDYPPEPTVSVNSGALTSGVHTTFAVLQ 180

Qy 178 SSGLYSLSSVVTVSSSLGTQTYICNVNHPKSNKTKVDKVPKSCDKTHTCPCPAPELL 237  
Db 181 SSGLYSLSSVVTVSSSLGTQTYICNVNHPKSNKTKVDKVPKSCDKTHTCPCPAPELL 240  
Qy 238 GGPSVFLFPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297  
Db 241 GGPSVFLFPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300  
Qy 298 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYVTLPPSR 357  
Db 301 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYVTLPPSR 360  
Qy 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKS 417  
Db 361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKS 420  
Qy 418 RMOQGNVFCVSNVHEALHNHYTQKSLSLSPGK 449  
Db 421 RMOQGNVFCVSNVHEALHNHYTQKSLSLSPGK 452

## RESULT 3

US-09-121-952A-71  
; Sequence 71, Application US/09121952A  
; Patent No. 6458355  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc., Hsai, Vanessa  
; APPLICANT: Koumenis, Iphigenia  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Shahrokh, Zahra  
; APPLICANT: Zapata, Gerardo A.  
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES  
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/121,952A  
; FILING DATE: 24-Jul-1998  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/074330  
; FILING DATE: 22-JAN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/075467  
; FILING DATE: 20-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 452 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-121-952A-71

Query Match 71.5%; Score 2194.5; DB 4; Length 452;  
Best Local Similarity 90.9%; Pred. No. 2.5e-161;

Matches 411; Conservative 14; Mismatches 24; Indels 3; Gaps 1;  
Qy 1 EVOLVESGGDFVOPGGSLRVSCAAGFAPFASHYAMVROAPGKLEWVAYISSGGSTYY 60  
Db 1 EVOLVSGGGLVOPGGSLRLSCAASGYSPSSHMHVWRQAPGKLEWVGVIDPSNGETTY 60  
Qy 61 SDSVKGRFTISRDNKNTLYLQWRSRAEDSAVYFCRTVKL---GTYYPDSWGGTLLTV 117  
Db 61 NQPKFKRFTLSRDNSKNTAYLQWNSRAEDTAVYVCARGDYRYNGDWFFPDVWGQGLTVTV 120  
Qy 118 SSASTKGPSVFLFPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 177  
Db 121 SSASTKGPSVFLFPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 180  
Qy 178 SSGLYSLSSVVTVSSSLGTQTYICNVNHPKSNKTKVDKVPKSCDKTHTCPCPAPELL 237  
Db 181 SSGLYSLSSVVTVSSSLGTQTYICNVNHPKSNKTKVDKVPKSCDKTHTCPCPAPELL 240  
Qy 238 GGPSVFLFPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297  
Db 241 GGPSVFLFPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300  
Qy 298 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYVTLPPSR 357  
Db 301 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYVTLPPSR 360  
Qy 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKS 417  
Db 361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKS 420  
Qy 418 RMOQGNVFCVSNVHEALHNHYTQKSLSLSPGK 449  
Db 421 RMOQGNVFCVSNVHEALHNHYTQKSLSLSPGK 452

RESULT 4  
US-09-234-340A-71  
; Sequence 71, Application US/09234340A  
; Patent No. 6468532  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc., Hsai, Vanessa  
; APPLICANT: Koumenis, Iphigenia  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Shahrokh, Zahra  
; APPLICANT: Zapata, Gerardo A.  
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES  
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/234,340A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/121,952  
; FILING DATE: 24-Jul-1998  
; APPLICATION NUMBER: 60/074330  
; FILING DATE: 22-JAN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/075467  
; FILING DATE: 20-FEB-1998

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-234-340A-71

Query Match      71.5%; Score 2194.5; DB 4; Length 452;
Best Local Similarity 90.9%; Pred. No. 2.5e-161;
Matches 411; Conservative 14; Mismatches 24; Indels 3; Gaps 1;

QY 1 EVQLVESGGDFVQPGGSLRVSFAASGFAFHYAMSVWRQAPGKLEWVAYISSGGSGTY 60
DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWRQAPGKLEWVGIIDPSNGETTY 60
. QY 61 SDSVKGRFTISRDNKNTLYLQMSRLRAEDSAVYFCTRVK---GTYVFDSSGQGLTIV 117
DB 61 NQKFKGRFTLSRDNSKNTAYLQWNSLRAEDTAVYICARGDYRNGDWFVVGQGLTIV 120
QY 118 SASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQ 177
DB 121 SASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQ 180
QY 178 SGLVSLSSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTCCPCPAPELL 237
DB 181 SGLVSLSSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTCCPCPAPELL 240
QY 238 GGPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQ 297
DB 241 GGPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQ 300
QY 298 YNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSR 357
DB 301 YNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSR 360
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 417
DB 361 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 420
QY 418 RQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
DB 421 RQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452

RESULT 5
US-08-157-101A-7
; Sequence 7, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBc ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157.101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-157-101A-7

Query Match      71.5%; Score 2194.5; DB 1; Length 459;
Best Local Similarity 91.8%; Pred. No. 2.5e-161;
Matches 413; Conservative 15; Mismatches 21; Indels 1; Gaps 1;

QY 1 EVQLVESGGDFVQPGGSLRVSFAASGFAFHYAMSVWRQAPGKLEWVAYISSGGSGTY 60
DB 10 QVQLVESGGVQVQPGSLRLSCAASGFTFSSNSMHWVRQAPGKLEWAVILYDGNHKFY 69
QY 61 SDSVKGRFTISRDNKNTLYLQMSRLRAEDSAVYFCTRVK-LGTYVFDSSGQGLTIVSS 119
DB 70 ADSVKGRFTISRDNKNTLYLQMSRLRAEDSAVYFCTRVK-LGTYVFDSSGQGLTIVSS 129
QY 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLOSS 179
DB 130 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLOSS 189
QY 180 GLYSLSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTCCPCPAPELLGG 239
DB 190 GLYSLSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTCCPCPAPELLGG 249
QY 240 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQYN 299
DB 250 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQYN 309
QY 300 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 359
DB 310 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 369
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 419
DB 370 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 429
QY 420 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
DB 430 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 459

RESULT 6
US-08-466-151-8
; Sequence 8, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: JARDIEU, Paula M.
; APPLICANT: PRESTA, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA way
```

CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,151  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/466163  
FILING DATE: 06-Jun-1995  
APPLICATION NUMBER: 08/405617  
FILING DATE: 15-MAR-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/185899  
FILING DATE: 26-JAN-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/879495  
FILING DATE: 07-MAY-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718P2C1D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO. 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 453 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-466-151-8

Query Match 70.6%; Score 2169; DB 3; Length 453;  
Best Local Similarity 91.0%; Pred. No. 2.3e-159;  
Matches 413; Conservative 16; Mismatches 19; Indels 6; Gaps 4;  
Qy 1 EVOLVESGGDFVQPGGSLRVSCAASGFAF--SHYAMSVVRQAPGKLEWVAYISSGSGTY 59  
Db 1 EVOLVESGGGLVQPGGSLRSLSCAVSGYSITSGYSWNWIRQAPGKLEWVASITYDGS-TN 59  
Qy 60 YSDSVKGRFTISRDNKNTLYLQWRSRLRAEDSAVYFCTRVK--LGTYYPDSWGQGLTLTV 117  
Db 60 YADSVKGRFTISRDDSKNTFYLQWNSLRAEDTAVYTCARGSHYFGHWFAVWQGLTVTV 119  
Qy 118 SSAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWGALTSVGHVTPAV 175  
Db 120 SSASTKGKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWGALTSVGHVTPAV 179  
Qy 176 LQSSGLYSLSSVTVPSSTSGTQTYICNVNHPKSNPKVDKVPKSCDKTHTCPCPAPE 235  
Db 180 LQSSGLYSLSSVTVPSSTSGTQTYICNVNHPKSNPKVDKVPKSCDKTHTCPCPAPE 239  
Qy 236 LLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 295  
Db 240 LLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 299  
Qy 296 EQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355  
Db 300 EQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359  
Qy 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415  
Db 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419

RESULT 8  
US-09-802-096-8  
; Sequence 8, Application US/09802096

Qy 416 KSRWQGNVFCSCVMHEALHNHYTKSLSPGK 449  
Db 420 KSRWQGNVFCSCVMHEALHNHYTKSLSPGK 453

RESULT 7  
US-08-466-163B-8  
; Sequence 8, Application US/08466163B  
; Patent No. 6329509  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; FILE REFERENCE: P0718P2C1D1  
; CURRENT APPLICATION NUMBER: US/08/466,163B  
; CURRENT FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 8  
; LENGTH: 453  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized mae11, version 1 heavy chain  
US-08-466-163B-8

Query Match 70.6%; Score 2169; DB 3; Length 453;  
Best Local Similarity 91.0%; Pred. No. 2.3e-159;  
Matches 413; Conservative 16; Mismatches 19; Indels 6; Gaps 4;  
Qy 1 EVOLVESGGDFVQPGGSLRVSCAASGFAF--SHYAMSVVRQAPGKLEWVAYISSGSGTY 59  
Db 1 EVOLVESGGGLVQPGGSLRSLSCAVSGYSITSGYSWNWIRQAPGKLEWVASITYDGS-TN 59  
Qy 60 YSDSVKGRFTISRDNKNTLYLQWRSRLRAEDSAVYFCTRVK--LGTYYPDSWGQGLTLTV 117  
Db 60 YADSVKGRFTISRDDSKNTFYLQWNSLRAEDTAVYTCARGSHYFGHWFAVWQGLTVTV 119  
Qy 118 SSAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWGALTSVGHVTPAV 175  
Db 120 SSASTKGKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWGALTSVGHVTPAV 179  
Qy 176 LQSSGLYSLSSVTVPSSTSGTQTYICNVNHPKSNPKVDKVPKSCDKTHTCPCPAPE 235  
Db 180 LQSSGLYSLSSVTVPSSTSGTQTYICNVNHPKSNPKVDKVPKSCDKTHTCPCPAPE 239  
Qy 236 LLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 295  
Db 240 LLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 299  
Qy 296 EQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355  
Db 300 EQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359  
Qy 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415  
Db 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419  
Qy 416 KSRWQGNVFCSCVMHEALHNHYTKSLSPGK 449  
Db 420 KSRWQGNVFCSCVMHEALHNHYTKSLSPGK 453



ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,352B  
FILING DATE: 03-Jul-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P1123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 451 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-887-352B-14

Query Match 70.6%; Score 2167; DB 2; Length 451;  
Best Local Similarity 90.9%; Pred. No. 3.3e-159;  
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;

QY 1 EVQLVESGGDVQPGGSLRVSCAASGFAP-SHYAMSVVRQAPGKGLWVAYISSGGSGTY 59  
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWMWIRQAPGKGLWVASITYDGS-TN 59  
QY 60 YSDSVKGRFTISRDNSKNTLYLQMSRLRAEDSAVYFCFTRVK--LGTYYFDSWGQGLT 117  
DB 60 YNPVKGRITISRDDSKNTFLQMSRLRAEDTAVYFCARGSHYFGHHFAVWGQGLT 119  
QY 118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 177  
DB 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 179  
QY 178 SSGLYSLSSVTVVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPE 237  
DB 180 SSGLYSLSSVTVVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPE 239  
QY 238 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEHNAKTKPREEQ 297  
DB 240 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEHNAKTKPREEQ 299  
QY 298 YNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357  
DB 300 YNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359  
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKS 417  
DB 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKS 419  
QY 418 RWOQGNVFCFSVMHEALHNHYTQKSLSLSPGK 449  
DB 420 RWOQGNVFCFSVMHEALHNHYTQKSLSLSPGK 451

RESULT 11

US-08-887-352B-16  
Sequence 16, Application US/08887352B  
Patent No. 5994511  
GENERAL INFORMATION:  
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
TITLE OF INVENTION: Improving Polypeptides  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way

CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,352B  
FILING DATE: 03-Jul-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P1123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 451 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-887-352B-16

Query Match 70.6%; Score 2167; DB 2; Length 451;  
Best Local Similarity 90.9%; Pred. No. 3.3e-159;  
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;

QY 1 EVQLVESGGDVQPGGSLRVSCAASGFAP-SHYAMSVVRQAPGKGLWVAYISSGGSGTY 59  
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWMWIRQAPGKGLWVASITYDGS-TN 59  
QY 60 YSDSVKGRFTISRDNSKNTLYLQMSRLRAEDSAVYFCFTRVK--LGTYYFDSWGQGLT 117  
DB 60 YNPVKGRITISRDDSKNTFLQMSRLRAEDTAVYFCARGSHYFGHHFAVWGQGLT 119  
QY 118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 177  
DB 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 179  
QY 178 SSGLYSLSSVTVVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPE 237  
DB 180 SSGLYSLSSVTVVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPE 239  
QY 238 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEHNAKTKPREEQ 297  
DB 240 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEHNAKTKPREEQ 299  
QY 298 YNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357  
DB 300 YNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359  
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKS 417  
DB 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKS 419  
QY 418 RWOQGNVFCFSVMHEALHNHYTQKSLSLSPGK 449  
DB 420 RWOQGNVFCFSVMHEALHNHYTQKSLSLSPGK 451

RESULT 12

US-08-466-151-65  
Sequence 65, Application US/08466151  
Patent No. 6037453  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 65



;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Genentech, Inc.  
;; STREET: 1 DNA Way  
;; CITY: South San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94080  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WinPatIn (Genentech)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/466,151  
;; FILING DATE:

;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/466163  
;; FILING DATE: 06-Jun-1995  
;; APPLICATION NUMBER: 08/405617  
;; FILING DATE: 15-MAR-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/185899  
;; FILING DATE: 26-JAN-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/879495  
;; FILING DATE: 07-MAY-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/744768  
;; FILING DATE: 14-AUG-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Svoboda, Craig G.  
;; REGISTRATION NUMBER: 39,044  
;; REFERENCE/DOCKET NUMBER: P0718P2C1D1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650/225-1489  
;; TELEFAX: 650/952-9881  
;; INFORMATION FOR SEQ ID NO: 65:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 451 amino acids  
;; TYPE: Amino Acid  
;; TOPOLOGY: Linear  
US-08-466-151-65

Query Match 70.6%; Score 2167; DB 3; Length 451;  
Best Local Similarity 90.9%; Pred. No. 3.3e-159;  
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;  
QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAP-SHYAMSVVROAPGKGLEWVAYISSGGSGTY 59  
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGS-TN 59  
QY 60 YSDSVKGRFTISRDNKNTLYLQMSRLRAEDSAVYFCTRVK--LGTYYPDSWGQGTLLTV 117  
DB 60 YNPYSVKGRITISRDDSKNTFYLQMSRLRAEDTAVYVCARGSHYFGHHFVAVWGQGTLLTV 119  
QY 118 SSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYKPEPTVVSWNSGALTSGVHTTTPAVLQ 177  
DB 120 SSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYKPEPTVVSWNSGALTSGVHTTTPAVLQ 179  
QY 178 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKHTCTCPCPAPELL 237  
DB 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKHTCTCPCPAPELL 239  
QY 238 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297  
DB 240 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299  
QY 298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQRPQVYTLPPSR 357  
DB 300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQRPQVYTLPPSR 359  
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFFLYSKLTVDK 417  
DB 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFFLYSKLTVDK 419  
QY 418 RWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 449  
DB 420 RWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 14  
US-09-109-207C-16  
; Sequence 16, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:

;;  
DB 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFFLYSKLTVDK 419  
QY 418 RWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 449  
DB 420 RWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 451  
RESULT 13  
US-09-109-207C-14  
; Sequence 14, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; CURRENT FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 14  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial  
; LOCATION: 1-451  
; OTHER INFORMATION: Heavy chain sequence derived from MAE11  
US-09-109-207C-14

Query Match 70.6%; Score 2167; DB 3; Length 451;  
Best Local Similarity 90.9%; Pred. No. 3.3e-159;  
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;  
QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAP-SHYAMSVVROAPGKGLEWVAYISSGGSGTY 59  
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGS-TN 59  
QY 60 YSDSVKGRFTISRDNKNTLYLQMSRLRAEDSAVYFCTRVK--LGTYYPDSWGQGTLLTV 117  
DB 60 YNPYSVKGRITISRDDSKNTFYLQMSRLRAEDTAVYVCARGSHYFGHHFVAVWGQGTLLTV 119  
QY 118 SSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYKPEPTVVSWNSGALTSGVHTTTPAVLQ 177  
DB 120 SSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYKPEPTVVSWNSGALTSGVHTTTPAVLQ 179  
QY 178 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKHTCTCPCPAPELL 237  
DB 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKHTCTCPCPAPELL 239  
QY 238 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297  
DB 240 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299  
QY 298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQRPQVYTLPPSR 357  
DB 300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQRPQVYTLPPSR 359  
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFFLYSKLTVDK 417  
DB 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFFLYSKLTVDK 419  
QY 418 RWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 449  
DB 420 RWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 451  
RESULT 14  
US-09-109-207C-16  
; Sequence 16, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:



APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
FILE REFERENCE: P1123R1  
CURRENT APPLICATION NUMBER: US/09/109,207C  
CURRENT FILING DATE: 1998-06-30  
PRIOR APPLICATION NUMBER: US 60/051,554  
PRIOR FILING DATE: 1997-07-03  
NUMBER OF SEQ ID NOS: 44  
SEQ ID NO 16  
LENGTH: 451  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
NAME/KEY: Artificial  
LOCATION: 1-451  
OTHER INFORMATION: Heavy chain sequence derived from MAE11  
US-09-109-207C-16

Query Match 70.6%; Score 2167; DB 3; Length 451;  
Best Local Similarity 90.9%; Pred. No. 3.3e-159;  
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;

Qy 1 EVOLVESGGDFVOPGGSLRVSCAASGAPF-SHYAMSHVROAPGKLEWVAYISGGSGTY 59  
Db 1 EVOLVESGGGLVOPGGSLRLSCAVSGYSITSGYSWNIROAPGKLEWVASITYDGS-TN 59  
Qy 60 YSDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCYTRVK--LGTYYFDSWGQGLTLTV 117  
Db 60 YNPSVKGRTISRDDSKNTFYLOMNSLRAEDTAVYICARGSHYFGHHFAVWGQGLTLTV 119  
Qy 118 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 177  
Db 120 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 179  
Qy 178 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELL 237  
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELL 239  
Qy 238 GGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297  
Db 240 GGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299  
Qy 298 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357  
Db 300 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359  
Qy 358 DELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKS 417  
Db 360 EEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKS 419  
Qy 418 RWQGNVFCSCVMHEALHNNHYTKSLSLSPGK 449  
Db 420 RWQGNVFCSCVMHEALHNNHYTKSLSLSPGK 451

RESULT 15  
US-09-296-005-14  
Sequence 14. Application US/09296005  
Patent No. 6290957  
GENERAL INFORMATION:  
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides  
FILE REFERENCE: P1123C1r  
CURRENT APPLICATION NUMBER: US/09/296,005  
CURRENT FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 08/887,352  
EARLIER FILING DATE: 1997-07-02  
NUMBER OF SEQ ID NOS: 26  
SEQ ID NO 14  
LENGTH: 451  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:

NAME/KEY: Artificial  
LOCATION: 1-451  
OTHER INFORMATION: Heavy chain sequence derived from MAE11  
US-09-296-005-14

Query Match 70.6%; Score 2167; DB 3; Length 451;  
Best Local Similarity 90.9%; Pred. No. 3.3e-159;  
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;

Qy 1 EVOLVESGGDFVOPGGSLRVSCAASGAPF-SHYAMSHVROAPGKLEWVAYISGGSGTY 59  
Db 1 EVOLVESGGGLVOPGGSLRLSCAVSGYSITSGYSWNIROAPGKLEWVASITYDGS-TN 59  
Qy 60 YSDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCYTRVK--LGTYYFDSWGQGLTLTV 117  
Db 60 YNPSVKGRTISRDDSKNTFYLOMNSLRAEDTAVYICARGSHYFGHHFAVWGQGLTLTV 119  
Qy 118 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 177  
Db 120 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 179  
Qy 178 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELL 237  
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELL 239  
Qy 238 GGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297  
Db 240 GGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299  
Qy 298 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357  
Db 300 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359  
Qy 358 DELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKS 417  
Db 360 EEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKS 419  
Qy 418 RWQGNVFCSCVMHEALHNNHYTKSLSLSPGK 449  
Db 420 RWQGNVFCSCVMHEALHNNHYTKSLSLSPGK 451

Search completed: August 1, 2005, 09:20:52  
Job time : 46.1842 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 1, 2005, 09:02:01 ; Search time 153.558 Seconds  
(without alignments)  
1476.651 Million cell updates/sec

Title: US-10-089-500-53

Perfect score: 3071

Sequence: 1 EVQLVESGGDFVQPGSLRV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:\*

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21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2750.5	89.6	579	14	US-10-138-727A-41
2	2750.5	89.6	579	14	US-10-310-719-32
3	2719.5	88.6	575	16	US-10-737-208A-6
4	2621	85.3	580	14	US-10-310-719-37
5	2589	84.3	580	14	US-10-310-719-35
6	2246.5	73.2	447	15	US-10-474-832-4
7	2240.5	73.0	447	15	US-10-474-832-5
8	2238.5	72.9	463	15	US-10-412-406-32
9	2238.5	72.9	4852	15	US-10-412-406-33
10	2236.5	72.8	447	15	US-10-474-832-6
11	2236	72.8	464	17	US-10-938-353-102
					Sequence 41, Appl
					Sequence 32, Appl
					Sequence 6, Appl
					Sequence 37, Appl
					Sequence 35, Appl
					Sequence 4, Appl
					Sequence 5, Appl
					Sequence 32, Appl
					Sequence 33, Appl
					Sequence 6, Appl
					Sequence 102, Appl

12	2234.5	72.8	445	14	US-10-320-231A-79	Sequence 79, Appl
13	2234.5	72.8	445	17	US-10-867-506-79	Sequence 79, Appl
14	2233	72.7	449	17	US-10-476-265-12	Sequence 12, Appl
15	2233	72.7	468	17	US-10-476-265-20	Sequence 20, Appl
16	2231.5	72.7	444	14	US-10-150-475A-6	Sequence 6, Appl
17	2231.5	72.7	444	16	US-10-704-522-6	Sequence 6, Appl
18	2231.5	72.7	444	16	US-10-645-215-6	Sequence 6, Appl
19	2229	72.6	470	17	US-10-938-353-98	Sequence 98, Appl
20	2226	72.5	449	9	US-09-736-371B-21	Sequence 21, Appl
21	2226	72.5	449	15	US-10-463-442-21	Sequence 21, Appl
22	2222.5	72.4	477	15	US-10-291-265-395	Sequence 395, Appl
23	2221.5	72.3	446	15	US-10-408-901-38	Sequence 38, Appl
24	2220	72.3	474	10	US-09-848-832-3	Sequence 3, Appl
25	2220	72.3	474	14	US-10-225-108A-3	Sequence 1, Appl
26	2220	72.3	474	15	US-10-461-148-1	Sequence 1, Appl
27	2216.5	72.2	442	15	US-10-226-435A-12	Sequence 12, Appl
28	2216.5	72.2	442	16	US-10-487-326-12	Sequence 12, Appl
29	2216.5	72.2	442	16	US-10-486-908-12	Sequence 12, Appl
30	2216.5	72.2	442	18	US-10-512-527-12	Sequence 12, Appl
31	2216	72.2	451	9	US-09-822-698A-26	Sequence 26, Appl
32	2215	72.1	449	17	US-10-985-584-10	Sequence 10, Appl
33	2212	72.0	445	15	US-10-408-901-34	Sequence 34, Appl
34	2209.5	71.9	442	16	US-10-487-322-12	Sequence 12, Appl
35	2209.5	71.9	442	16	US-10-487-326-21	Sequence 21, Appl
36	2209.5	71.9	442	16	US-10-486-908-16	Sequence 16, Appl
37	2209.5	71.9	442	18	US-10-512-527-21	Sequence 21, Appl
38	2207	71.9	453	17	US-10-891-658-41	Sequence 41, Appl
39	2202.5	71.7	446	15	US-10-408-901-46	Sequence 46, Appl
40	2202.5	71.7	469	16	US-10-858-186-14	Sequence 14, Appl
41	2198.5	71.6	469	15	US-10-656-769-26	Sequence 26, Appl
42	2195	71.5	445	15	US-10-408-901-42	Sequence 42, Appl
43	2194.5	71.5	452	10	US-09-726-258-71	Sequence 71, Appl
44	2193.5	71.4	452	17	US-10-861-049-46	Sequence 46, Appl
45	2192.5	71.4	469	15	US-10-656-769-20	Sequence 20, Appl
46	2191	71.3	474	15	US-10-108-260A-4640	Sequence 4640, Appl
47	2191	71.3	713	16	US-10-679-620-64	Sequence 64, Appl
48	2191	71.3	715	16	US-10-679-620-62	Sequence 62, Appl
49	2190.5	71.3	448	17	US-10-985-584-18	Sequence 18, Appl
50	2190.5	71.3	452	16	US-10-818-765-4	Sequence 4, Appl
51	2190.5	71.3	452	17	US-10-861-049-16	Sequence 16, Appl
52	2190.5	71.3	471	17	US-10-877-363-4	Sequence 4, Appl
53	2190.5	71.3	471	17	US-10-922-651-4	Sequence 4, Appl
54	2190.5	71.3	471	17	US-10-861-049-4	Sequence 4, Appl
55	2186.5	71.2	446	15	US-10-408-901-30	Sequence 30, Appl
56	2185.5	71.2	446	15	US-10-408-901-50	Sequence 50, Appl
57	2184.5	71.1	447	16	US-10-379-392-116	Sequence 116, Appl
58	2183.5	71.1	447	16	US-10-379-392-117	Sequence 117, Appl
59	2181.5	71.0	452	17	US-10-861-049-22	Sequence 22, Appl
60	2181	71.0	451	15	US-10-423-299-4	Sequence 4, Appl
61	2180.5	71.0	447	16	US-10-379-392-119	Sequence 119, Appl
62	2175.5	70.8	447	16	US-10-029-988B-26	Sequence 26, Appl
63	2175.5	70.8	447	16	US-10-032-423A-26	Sequence 26, Appl
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66	2173	70.8	471	17	US-10-861-049-11	Sequence 11, Appl
67	2173	70.8	464	15	US-10-032-037B-26	Sequence 26, Appl
68	2173	70.8	464	15	US-10-029-988B-26	Sequence 26, Appl
69	2173	70.8	464	15	US-10-032-423A-26	Sequence 26, Appl
70	2172	70.7	472	15	US-10-029-926B-26	Sequence 26, Appl
71	2169	70.6	449	16	US-10-108-260A-4073	Sequence 4073, Appl
72	2169	70.6	449	16	US-10-635-908-16	Sequence 16, Appl
73	2169	70.6	453	9	US-09-802-077-8	Sequence 8, Appl
74	2169	70.6	453	9	US-09-802-096-8	Sequence 8, Appl
75	2169	70.6	453	10	US-09-925-179-8	Sequence 8, Appl
76	2169	70.6	453	17	US-10-968-237-8	Sequence 14, Appl
77	2167	70.6	451	9	US-09-920-171-16	Sequence 16, Appl
78	2167	70.6	451	9	US-09-920-171-16	Sequence 16, Appl
79	2167	70.6	451	10	US-09-925-179-65	Sequence 65, Appl
80	2167	70.6	451	14	US-10-113-996-14	Sequence 14, Appl
81	2167	70.6	451	14	US-10-113-996-14	Sequence 14, Appl
82	2167	70.6	451	16	US-10-813-483-4	Sequence 4, Appl
83	2167	70.6	451	16	US-10-813-483-5	Sequence 5, Appl
84	2167	70.6	451	16	US-10-791-619-14	Sequence 14, Appl

85 2167 70.6 451 16 US-10-791-619-16 Sequence 16, Appli  
86 2167 70.6 451 17 US-10-714-000-2 Sequence 2, Appli  
87 2167 70.6 451 17 US-10-698-073-9 Sequence 9, Appli  
88 2167 70.6 451 17 US-10-968-237-65 Sequence 65, Appli  
89 2167 70.6 451 20 US-11-013-966-4 Sequence 4, Appli  
90 2167 70.6 451 20 US-11-013-966-5 Sequence 5, Appli  
91 2167 70.6 476 14 US-10-020-786-11 Sequence 11, Appli  
92 2167 70.6 476 17 US-10-697-995-9 Sequence 9, Appli  
93 2167 70.6 667 16 US-10-764-428-7 Sequence 7, Appli  
94 2167 70.6 669 16 US-10-764-428-21 Sequence 21, Appli  
95 2166.5 70.5 447 16 US-10-379-392-143 Sequence 143, App  
96 2165 70.5 451 17 US-10-698-073-7 Sequence 7, Appli  
97 2164 70.5 451 10 US-09-925-179-66 Sequence 66, Appli  
98 2164 70.5 451 17 US-10-968-237-66 Sequence 66, Appli  
99 2163 70.4 451 9 US-09-920-171-18 Sequence 18, Appli  
100 2163 70.4 451 10 US-09-792-938-2 Sequence 2, Appli

## ALIGNMENTS

## RESULT 1

US-10-138-727A-41  
; Sequence 41, Application US/10138727A  
; Publication No. US20030157054A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Qian, Susan  
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
; FILE REFERENCE: LEX-019  
; CURRENT APPLICATION NUMBER: US/10/138,727A  
; CURRENT FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: US 60/288,564  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 41  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: heavy chain-IL2  
US-10-138-727A-41

Query Match 89.6%; Score 2750.5; DB 14; Length 579;  
Best Local Similarity 88.5%; Pred. No. 6.4e-166;  
Matches 516; Conservative 32; Mismatches 30; Indels 5; Gaps 2;

QY 1 EVLVESGDDFVQPGSLRVSCAASGFAPSHYAMSWVRQAPGKGLWYAYISSGSGGTYY 60  
DB 1 QIQLVQSGAEVKKPGETIKISKDASGYFTTNYGMNVRQTPGKGLKMMGWINTYTGPTY 60  
QY 61 SDSVKGRTTISRDNSKNTLYLQMRSLRAEDSAVYFCTR-VKLGTYVYFDSWGGTLLTVSS 119  
DB 61 ADDFKGRFTTIAETSTSTLYLQNLNRSDEDTATYFCVRFISKGDY----WGQGTVTYVSS 116  
QY 120 ASTKGPSVFPFLAPSSKTSGGTAALGCLVKDYFPEPTVWMSNGALTSGVHTFPAVLQSS 179  
DB 61 ADDFKGRFTTIAETSTSTLYLQNLNRSDEDTATYFCVRFISKGDY----WGQGTVTYVSS 116  
QY 180 GLYSLSVVTVVPSLSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHKTPCPAPPELLGG 239  
DB 177 GLYSLSVVTVVPSLSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHKTPCPAPPELLGG 236  
QY 240 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNAKTKPREEQYN 299  
DB 237 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNAKTKPREEQYN 296  
QY 300 STYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDE 359  
DB 297 STYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDE 356

QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419  
DB 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 416  
QY 420 QGQNVFSCVMHEALHNNHYTKSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLNGINN 479  
DB 417 QGQNVFSCVMHEALHNNHYTKSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLNGINN 476  
QY 480 YKNPKLTMLTKFPMFKKATLKHLCLEBELKPLEEVNLNAQSKNHLRPRDLISIN 539  
DB 477 YKNPKLTMLTKFPMFKKATLKHLCLEBELKPLEEVNLNAQSKNHLRPRDLISIN 536  
QY 540 VIVLELKSETFMECEYADETATIVFELNRMITFCQSIISTLT 582  
DB 537 VIVLELKSETFMECEYADETATIVFELNRMITFCQSIISTLT 579

## RESULT 2

US-10-310-719-32  
; Sequence 32, Application US/10310719  
; Publication No. US20030166163A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity  
; FILE REFERENCE: LEX-020  
; CURRENT APPLICATION NUMBER: US/10/310,719  
; CURRENT FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/337,113  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/371,966  
; PRIOR FILING DATE: 2002-04-12  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: di-KS-ala IL2 (D20T) heavy chain fused to IL-2 variant  
US-10-310-719-32

Query Match 89.6%; Score 2750.5; DB 14; Length 579;  
Best Local Similarity 88.5%; Pred. No. 6.4e-166;  
Matches 516; Conservative 32; Mismatches 30; Indels 5; Gaps 2;

QY 1 EVLVESGDDFVQPGSLRVSCAASGFAPSHYAMSWVRQAPGKGLWYAYISSGSGGTYY 60  
DB 1 QIQLVQSGPELKKPGSSVKISKASGYFTTNYGMNVRQAPGKGLKMMGWINTYTGPTY 60  
QY 61 SDSVKGRTTISRDNSKNTLYLQMRSLRAEDSAVYFCTR-VKLGTYVYFDSWGGTLLTVSS 119  
DB 61 ADDFKGRFTTIAETSTSTLYLQNLNRSDEDTATYFCVRFISKGDY----WGQGTVTYVSS 116  
QY 120 ASTKGPSVFPFLAPSSKTSGGTAALGCLVKDYFPEPTVWMSNGALTSGVHTFPAVLQSS 179  
DB 117 ASTKGPSVFPFLAPSSKTSGGTAALGCLVKDYFPEPTVWMSNGALTSGVHTFPAVLQSS 176  
QY 180 GLYSLSVVTVVPSLSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHKTPCPAPPELLGG 239  
DB 177 GLYSLSVVTVVPSLSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHKTPCPAPPELLGG 236  
QY 240 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNAKTKPREEQYN 299  
DB 237 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNAKTKPREEQYN 296  
QY 300 STYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDE 359  
DB 297 STYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDE 356  
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419  
DB 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 416

Qy 420 QQNVFSCVMHEALHNHYTKQSLSLSPGKAPTSSSTKTKTQLEHLLDQLMILNGINN 479  
Db 417 QQNVFSCVMHEALHNHYTKQSATATPGAAPTSSSTKTKTQLEHLLDQLMILNGINN 476  
Qy 480 YKNPKLTRMLTFKPYMPKKATELKHQCLEBELKPLEEVLNLAQSKNPHLRPRDLISNIN 539  
Db 477 YKNPKLTRMLTFKPYMPKKATELKHQCLEBELKPLEEVLNLAQSKNPHLRPRDLISNIN 536  
Qy 540 VIVLELKGSETTFMCEYADETATTFVEFLNRWITFCQSIISTLT 582  
Db 537 VIVLELKGSETTFMCEYADETATTFVEFLNRWITFCQSIISTLT 579  
RESULT 3  
US-10-737-208A-6  
; Sequence 6, Application US/10737208A  
; Publication No. US20040203100A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen D.  
; TITLE OF INVENTION: IMMUNOCYTOKINE SEQUENCES AND USES THEREOF  
; FILE REFERENCE: LEX-023  
; CURRENT APPLICATION NUMBER: US/10/737,208A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR FILING DATE: 2003-12-16  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 575  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized Immunoglobulin Heavy Chain-IL-2  
US-10-737-208A-6  
Query Match 88.6%; Score 2719.5; DB 16; Length 575;  
Best Local Similarity 89.0%; Pred. No. 5.8e-164;  
Matches 518; Conservative 24; Mismatches 33; Indels 7; Gaps 3;  
Qy 1 EVOLVSGGDFVQGGSLRVSCAASGAFSHYAMSWRQAPGKLEWVAYISSGSGTYY 60  
Db 1 EVOLVSGAGVERPGASVKLSCKASGSSFTGYNNWVRQNGIKSLEWIGADIPYGGTSY 60  
Qy 61 SDSVKGRFTISRDNKNTLYQMRSLRAEDSAVYFCTRVKLTGYTFDSWGQGLTLLTVSSA 120  
Db 61 NQKFGKATLTVDKSTSTAMHLKSLRSEDTAYVCVS---GNEY---WQGGTSVTVSSA 114  
Qy 121 STKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNGALTSGVHTFPAVLQSSG 180  
Db 115 STKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNGALTSGVHTFPAVLQSSG 174  
Qy 181 LYSLSVSVTVPSSSLGTQTYICNVNHPKSPNTKVDKVEPKSCDKTHTCPCPAPELLGGP 240  
Db 175 LYSLSVSVTVPSSSLGTQTYICNVNHPKSPNTKVDKVEPKSCDKTHTCPCPAPELLGGP 234  
Qy 241 SVFLFPPKPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS 300  
Db 235 SVFLFPPKPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS 294  
Qy 301 TYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDEL 360  
Db 295 TYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDEM 354  
Qy 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQ 420  
Db 355 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQ 414  
Qy 421 QGNVFCSCVMHEALHNHYTKQSLSLSPGKAPTSSSTKTKTQLEHLLDQLMILNGINN 480  
Db 415 QGNVFCSCVMHEALHNHYTKQSLSLSPG-APTSSSTKTKTQLEHLLDQLMILNGINN 473  
Qy 481 KNPKLTRMLTFKPYMPKKATELKHQCLEBELKPLEEVLNLAQSKNPHLRPRDLISNIN 540

Db 474 KNPKLTRMLTFKPYMPKKATELKHQCLEBELKPLEEVLNLAQSKNPHLRPRDLISNIN 533  
Qy 541 IVLELKGSETTFMCEYADETATTFVEFLNRWITFCQSIISTLT 582  
Db 534 IVLELKGSETTFMCEYADETATTFVEFLNRWITFCQSIISTLT 575  
RESULT 4  
US-10-310-719-37  
; Sequence 37, Application US/10310719  
; Publication No. US20030166163A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity  
; FILE REFERENCE: LEX-020  
; CURRENT APPLICATION NUMBER: US/10/310,719  
; CURRENT FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/337,113  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/371,966  
; PRIOR FILING DATE: 2002-04-12  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37  
; LENGTH: 580  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: dI-NHS76 (gamma4h) (FN>AQ)-aIa-IL2 (D20T) heavy chain fused to  
; OTHER INFORMATION: IL-2 variant  
US-10-310-719-37  
Query Match 85.1%; Score 2621; DB 14; Length 580;  
Best Local Similarity 85.8%; Pred. No. 1e-157;  
Matches 500; Conservative 29; Mismatches 50; Indels 4; Gaps 3;  
Qy 1 EVOLVSGGDFVQGGSLRVSCAASGAFSH-YAMSWRQAPGKLEWVAYISSGSGTYY 59  
Db 1 QVQLQSSGCLVKPKSETLSITCAVSCYSISSGYWGMIRQPPCKGLEWIGSIYHSGS-TY 59  
Qy 60 YDSVVKGRFTISRDNKNTLYQMRSLRAEDSAVYFCTRVKLTGYTFDSWGQGLTLLTVSS 119  
Db 60 YNPGLKSRVTISVDTSKQFSLKLSSTAAADTAATVYTCARGKSK--FDYWGQGLTLLTVSS 117  
Qy 120 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNGALTSGVHTFPAVLQSS 179  
Db 118 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNGALTSGVHTFPAVLQSS 177  
Qy 180 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSPNTKVDKVEPKSCDKTHTCPCPAPELLGG 239  
Db 178 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSPNTKVDKVEPKSCDKTHTCPCPAPELLGG 237  
Qy 240 PSVFLFPPKPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 299  
Db 238 PSVFLFPPKPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 297  
Qy 300 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 359  
Db 298 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 357  
Qy 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 419  
Db 358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 417  
Qy 420 QGNVFCSCVMHEALHNHYTKQSLSLSPGKAPTSSSTKTKTQLEHLLDQLMILNGINN 479  
Db 418 QGNVFCSCVMHEALHNHYTKSATATPGAAPTSSSTKTKTQLEHLLDQLMILNGINN 477  
Qy 480 YKNPKLTRMLTFKPYMPKKATELKHQCLEBELKPLEEVLNLAQSKNPHLRPRDLISNIN 539  
Db 478 YKNPKLTRMLTFKPYMPKKATELKHQCLEBELKPLEEVLNLAQSKNPHLRPRDLISNIN 537



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; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/283,794
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/303,689
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-10-474-832-5

Query Match          73.08; Score 2240.5; DB 15; Length 447;
Best Local Similarity 94.9%; Pred. No. 9.9e-134;
Matches 425; Conservative 4; Mismatches 18; Indels 1; Gaps 1;

Qy 1 EVLVESGGDFVOPGGSLRVSCAASGFASFHYAMSWVRQAPGKGLEWVAIISGGSGTY 60
Db 1 EVLVESGGGLVOPGGSLRVSCAASGFTFSRYTMSWVRQAPGKGLEWVAIISGGH-TYY 59

Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFDSWQGGTLTVSSA 120
Db 60 LDSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYCTRGFGDGYFDVWGQGLTVTVSSA 119

Qy 121 STKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 180
Db 120 STKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 179

Qy 181 LYSLSVSVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTHTCPCPAPELLGGP 240
Db 180 LYSLSVSVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTHTCPCPAPELLGGP 239

Qy 241 SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREQYNS 300
Db 240 SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREQYQS 299

Qy 301 TYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDEL 360
Db 300 TYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDEL 359

Qy 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRWQ 420
Db 360 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRWQ 419

Qy 421 QGNVFSCVMHEALHNHYTQKSLSLSPG 448
Db 420 QGNVFSCVMHEALHNHYTQKSLSLSPG 447

RESULT 8
US-10-412-406-32
; Sequence 32, Application US/10412406
; Publication No. US20040058394A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: GARBER, Ellen
; APPLICANT: LYNE, Paul
; APPLICANT: SALDHANA, Jose W.
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
; FILE REFERENCE: BINALOOCN
; CURRENT APPLICATION NUMBER: US/10/412,406
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 60/240,285
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/275,289
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/299,987
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: PCT/US01/32140
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; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-412-406-32

Query Match          72.9%; Score 2238.5; DB 15; Length 663;
Best Local Similarity 94.0%; Pred. No. 2e-133;
Matches 422; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

Qy 1 EVLVESGGDFVOPGGSLRVSCAASGFASFHYAMSWVRQAPGKGLEWVAIISGGSGTY 60
Db 215 EVLVESGGGLVKPGGSLRVSCAASGFTFSYYWFRQAPGKGLEWVAIISGGSYTY 274

Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFDSWQGGTLTVSS 119
Db 275 PDSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYCARBENGNYFYFDYWGQGTTVTVSS 334

Qy 120 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 179
Db 335 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 394

Qy 180 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTHTCPCPAPELLGG 239
Db 395 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTHTCPCPAPELLGG 454

Qy 240 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREQYN 299
Db 455 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREQYN 514

Qy 300 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 359
Db 515 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 574

Qy 360 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 419
Db 575 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 634

Qy 420 QGNVFSCVMHEALHNHYTQKSLSLSPG 448
Db 635 QGNVFSCVMHEALHNHYTQKSLSLSPG 663

RESULT 9
US-10-412-406-33
; Sequence 33, Application US/10412406
; Publication No. US20040058394A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: GARBER, Ellen
; APPLICANT: LYNE, Paul
; APPLICANT: SALDHANA, Jose W.
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
; FILE REFERENCE: BINALOOCN
; CURRENT APPLICATION NUMBER: US/10/412,406
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 60/240,285
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/275,289
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/299,987
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: PCT/US01/32140
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 4852
; TYPE: PRT
; ORGANISM: Homo Sapien
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US-10-412-406-33

```
Query Match          72.9%; Score 2238.5; DB 15; Length 4852;
Best Local Similarity 94.0%; Pred. No. 2.1e-132;
Matches 422; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

QY 1 EVQLVESGGDFVQPGGSLRVSCAAGSPAFSHYAMSWRQAPGKLEWVAYISGGSGTYY 60
DB 4404 EVQLVESGGGLVQPGGSLRLSCAAGSFTFSDYIMTFWFRQAPGKLEWATISDGGSYTY 4463

QY 61 SDSVKGRTTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLG-YYFDSWGQGLTLLTVSS 119
DB 4464 PDSVKGRTTISRDNKNTLYLQMRSLRAEDTAVYICAREENGNFYFDYWGQGLTLLTVSS 4523

QY 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPPEVTVSWNSGALTSGVHTFPAVLQSS 179
DB 4524 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPEVTVSWNSGALTSGVHTFPAVLQSS 4583

QY 180 GLYSLSVVTVFPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGG 239
DB 4584 GLYSLSVVTVFPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGG 4643

QY 240 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
DB 4644 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 4703

QY 300 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
DB 4704 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 4763

QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSLKTVDKSRW 419
DB 4764 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSLKTVDKSRW 4823

QY 420 QGNVFSCSVMEALHNHYTQKSLSLSPG 448
DB 4824 QGNVFSCSVMEALHNHYTQKSLSLSPG 4852

RESULT 10
US-10-474-832-6
; Sequence 6, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: ANTIBODIES TO VLA-1
; FILE REFERENCE: A101 PCT
; CURRENT APPLICATION NUMBER: US/10/474,832
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/283,794
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/303,689
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-10-474-832-6

Query Match          72.8%; Score 2236.5; DB 15; Length 447;
Best Local Similarity 94.6%; Pred. No. 1.7e-133;
Matches 424; Conservative 4; Mismatches 19; Indels 1; Gaps 1;

QY 1 EVQLVESGGDFVQPGGSLRVSCAAGSPAFSHYAMSWRQAPGKLEWVAYISGGSGTYY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAAGSFTFSRYTMSWRQAPGKLEWATISGGGH-TYY 59

QY 61 SDSVKGRTTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYTFDSWGQGLTLLTVSSA 120
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DB 60 LDSVKGRTTISRDNKNTLYLQMRSLRAEDTAVYCTRGFGDGYFDYWGQGLTLLTVSSA 119
QY 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPPEVTVSWNSGALTSGVHTFPAVLQSSG 180
DB 120 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPEVTVSWNSGALTSGVHTFPAVLQSSG 179

QY 181 LYSLSVVTVFPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGP 240
DB 180 LYSLSVVTVFPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPAAAGP 239

QY 241 SVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
DB 240 SVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299

QY 301 TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
DB 300 TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359

QY 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSLKTVDKSRWQ 420
DB 360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSLKTVDKSRWQ 419

QY 421 QGNVFSCSVMEALHNHYTQKSLSLSPG 448
DB 420 QGNVFSCSVMEALHNHYTQKSLSLSPG 447

RESULT 11
US-10-938-353-102
; Sequence 102, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
; APPLICANT: FOLTZ, IAN
; APPLICANT: HAAK-FRENDSCHO, MARY
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: LOW, JOSEPH EDWIN
; APPLICANT: MOBLEY, JAMES LESLIE
; TITLE OF INVENTION: ANTIBODIES TO M-CSF
; FILE REFERENCE: ABX-PF4
; CURRENT APPLICATION NUMBER: US/10/938,353
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/502,163
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 102
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-353-102

Query Match          72.8%; Score 2236; DB 17; Length 464;
Best Local Similarity 93.5%; Pred. No. 1.9e-133;
Matches 420; Conservative 11; Mismatches 14; Indels 4; Gaps 1;

QY 1 EVQLVESGGDFVQPGGSLRVSCAAGSPAFSHYAMSWRQAPGKLEWVAYISGGSGTYY 60
DB 20 QVQLVESGGGLVQPGGSLRLSCAAGSFTFSDYIMSWIRQAPGKLEWVSYISSSGSTIYY 79

QY 61 SDSVKGRTTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYTFDSWGQGLTLLTVSSA 120
DB 80 ADSVKGRTTISRDNKNTLYLQMRSLRAEDTAVYICARGLTGDY---WGQGLTLLTVSSA 135

QY 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPPEVTVSWNSGALTSGVHTFPAVLQSSG 180
DB 136 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPEVTVSWNSGALTSGVHTFPAVLQSSG 195

QY 181 LYSLSVVTVFPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGP 240
DB 196 LYSLSVVTVFPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGP 255
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QY 241 SVFLPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300  
DB 256 SVFLPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 315  
QY 301 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISAKAGQPREPQVYTLPPSRDEL 360  
DB 316 TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISAKAGQPREPQVYTLPPSRDEL 375  
QY 361 TKQVSLTCLVKGFPYSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ 420  
DB 376 TKQVSLTCLVKGFPYSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ 435  
QY 421 QGNVFCVSMHEALHNHYTQKSLSLSPGK 449  
DB 436 QGNVFCVSMHEALHNHYTQKSLSLSPGK 464

RESULT 12  
US-10-320-231A-79  
; Sequence 79, Application US/10320231A  
; Publication No. US20030194405A1  
; GENERAL INFORMATION:  
; APPLICANT: Neben, Steven  
; APPLICANT: Takeuchi, Toshihiko  
; APPLICANT: Tomkinson, Adrian  
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For  
; TITLE OF INVENTION: Treatment Of Asthma  
; FILE REFERENCE: 7430\*163  
; CURRENT APPLICATION NUMBER: US/10/320,231A  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/342,174  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 79  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic sequence  
US-10-320-231A-79

Query Match 72.8%; Score 2234.5; DB 14; Length 445;  
Best Local Similarity 94.4%; Pred. No. 2.3e-133;  
Matches 421; Conservative 7; Mismatches 17; Indels 1; Gaps 1;  
QY 4 LVESGGDFVOPGSLRVSCAASGFATSHYAMSWVRQAPGKLEWVAIISGGSGTYSDS 63  
DB 1 LVESGGGLVOPGGSLRLSCLSAASGFTFSSVAMSWVRQAPGKLEWVAISGGSGTYADS 60  
QY 64 VKGRFTISRDNKNTLYLQMSLRADSDAVYFCTRVKLTGYTFDSNGQGTLLTVSSASTK 123  
DB 61 VKGRFTISRDNKNTLYLQMSLRADSDAVYFCTRVKLTGYTFDSNGQGTLLTVSSASTK 119  
QY 124 GPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSGLYS 183  
DB 120 GPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSGLYS 179  
QY 184 LSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKHTCTCPPELGGPSVF 243  
DB 180 LSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKHTCTCPPELGGPSVF 239  
QY 244 LPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 303  
DB 180 LSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKHTCTCPPELGGPSVF 239  
QY 244 LPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 303  
DB 240 LPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299  
QY 304 VVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISAKAGQPREPQVYTLPPSRDELTKN 363  
DB 240 LPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299  
QY 304 VVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISAKAGQPREPQVYTLPPSRDELTKN 363  
DB 300 VVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISAKAGQPREPQVYTLPPSRDELTKN 359  
QY 364 QVSLTCLVKGFPYSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ 423  
DB 300 VVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISAKAGQPREPQVYTLPPSRDELTKN 359  
QY 364 QVSLTCLVKGFPYSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ 423

DB 360 QVSLTCLVKGFPYSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ 419  
QY 424 VFLSCVMHEALHNHYTQKSLSLSPGK 449  
DB 420 VFLSCVMHEALHNHYTQKSLSLSPGK 445

RESULT 13  
US-10-867-506-79  
; Sequence 79, Application US/10867506  
; Publication No. US20050112698A1  
; GENERAL INFORMATION:  
; APPLICANT: Neben, Steven  
; APPLICANT: Takeuchi, Toshihiko  
; APPLICANT: Tomkinson, Adrian  
; APPLICANT: Delaria, Kathy  
; APPLICANT: Yan, Kelly  
; APPLICANT: Wong, Teresa  
; APPLICANT: Longphre, Malinda  
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For  
; TITLE OF INVENTION: Treatment Of Asthma  
; FILE REFERENCE: 11334\*10  
; CURRENT APPLICATION NUMBER: US/10/867,506  
; CURRENT FILING DATE: 2004-06-14  
; PRIOR APPLICATION NUMBER: US 10/320,231  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: US 60/342,174  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 79  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic sequence  
US-10-867-506-79

Query Match 72.8%; Score 2234.5; DB 17; Length 445;  
Best Local Similarity 94.4%; Pred. No. 2.3e-133;  
Matches 421; Conservative 7; Mismatches 17; Indels 1; Gaps 1;  
QY 4 LVESGGDFVOPGSLRVSCAASGFATSHYAMSWVRQAPGKLEWVAIISGGSGTYSDS 63  
DB 1 LVESGGGLVOPGGSLRLSCLSAASGFTFSSVAMSWVRQAPGKLEWVAISGGSGTYADS 60  
QY 64 VKGRFTISRDNKNTLYLQMSLRADSDAVYFCTRVKLTGYTFDSNGQGTLLTVSSASTK 123  
DB 61 VKGRFTISRDNKNTLYLQMSLRADSDAVYFCTRVKLTGYTFDSNGQGTLLTVSSASTK 119  
QY 124 GPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSGLYS 183  
DB 120 GPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSSGLYS 179  
QY 184 LSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKHTCTCPPELGGPSVF 243  
DB 180 LSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKHTCTCPPELGGPSVF 239  
QY 244 LPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 303  
DB 240 LPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299  
QY 304 VVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISAKAGQPREPQVYTLPPSRDELTKN 363  
DB 300 VVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISAKAGQPREPQVYTLPPSRDELTKN 359  
QY 364 QVSLTCLVKGFPYSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ 423  
DB 360 QVSLTCLVKGFPYSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ 419  
QY 424 VFLSCVMHEALHNHYTQKSLSLSPGK 449  
DB 420 VFLSCVMHEALHNHYTQKSLSLSPGK 445



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:58:15 ; Search time 32.9571 Seconds  
(without alignments)  
1699.125 Million cell updates/sec

Title: US-10-089-500-53

Perfect score: 3071

Sequence: 1 EVLVESGGDFVQPGSLRV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1767	57.5	330	1 GHU	Ig gamma-1 chain C
2	1630.5	53.1	377	2 A23511	Ig gamma-3 chain C
3	1628.5	53.0	377	2 A60764	Ig gamma-3 chain C
4	1604	52.2	326	1 G2HU	Ig gamma-2 chain C
5	1590.5	51.8	327	1 G4HU	Ig gamma-4 chain C
6	1508.5	49.1	444	2 PC4436	monoclonal antibod
7	1487	48.4	470	2 S22080	Ig heavy chain pre
8	1440.5	46.9	469	2 S37483	Ig gamma-2a chain
9	1437	46.8	446	2 S40295	Ig gamma-2a chain
10	1434	46.7	472	2 S31459	Ig gamma-1 chain -
11	1429	46.5	374	2 S69339	Ig heavy chain V r
12	1390	45.3	474	1 G2MS11	Ig gamma-2b chain
13	1367.5	44.5	475	2 S01321	Ig gamma-2b chain
14	1263	41.1	328	2 I47159	Ig gamma 2a chain
15	1260	41.0	255	4 S31866	Ig gamma-1 chain C
16	1257	40.9	328	2 I47160	Ig gamma 2b chain
17	1254	40.8	234	2 PT0207	Ig gamma chain C r
18	1231	40.1	328	2 I47158	Ig gamma 1 chain C
19	1230.5	40.1	323	1 GHRB	Ig gamma chain C r
20	1227	40.0	328	2 I47161	Ig gamma 3 chain C
21	1216.5	39.6	329	1 G2GP	Ig gamma-2 chain C
22	1161.5	37.8	308	2 C30554	Ig heavy chain C r
23	1152	37.5	326	2 PS0017	Ig gamma-1 chain C
24	1151	37.5	289	1 G3HUM1	Ig gamma-3 heavy c
25	1146.5	37.3	333	2 PS0018	Ig gamma-2b chain
26	1142	37.2	324	1 G1MS	Ig gamma-1 chain C
27	1141	37.2	329	1 G1MSC	Ig gamma-3 chain C
28	1139	37.1	393	1 G1MSM	Ig gamma-1 chain C
29	1130	36.8	398	1 G3MSM	Ig gamma-3 chain C

30	1126	36.7	330	1 G2MSA	Ig gamma-2a chain
31	1123.5	36.6	335	1 G2MSAB	Ig gamma-2a chain
32	1121	36.5	339	1 G2MSAM	Ig gamma-2a chain
33	1118.5	36.4	329	2 S00847	Ig gamma-2c chain
34	1112	36.2	322	2 PS0019	Ig gamma-2a chain
35	1102	35.9	548	2 S38864	Ig epsilon chain C
36	1092.5	35.6	327	2 G06611	Ig gamma-2 chain C
37	1082	35.2	405	1 G2MSBM	Ig gamma-2 chain C
38	1066	34.7	277	2 I47162	Ig gamma 4 chain c
39	866.5	28.2	549	2 S04845	Ig heavy chain pre
40	856.5	27.9	249	2 S69340	Ig heavy chain VHI
41	820.5	26.7	241	2 S69131	Ig heavy chain (DO
42	817.5	26.6	572	2 B46529	Ig y heavy chain (
43	810	26.4	218	2 A36040	Ig heavy chain V-I
44	792	25.8	220	2 A94444	Ig gamma-1 heavy c
45	750	24.4	246	2 S38950	Ig gamma chain - m
46	745.5	24.3	213	2 S68213	Ig heavy chain (Ma
47	745	24.3	627	2 S14683	Ig mu chain precu
48	727.5	23.7	254	2 B31790	Ig heavy chain V r
49	708.5	23.1	585	2 A46507	Ig alpha chain - c
50	707	23.0	180	2 I46732	Ig gamma heavy cha
51	690	22.5	153	1 ICG12	interleukin-2 prec
52	690	22.5	153	1 ICHU2	interleukin-2 prec
53	686.5	22.4	592	2 S25705	Ig mu chain - shee
54	681	22.2	220	2 S68211	Ig heavy chain (Ma
55	666.5	21.7	568	2 A34891	Ig heavy chain pre
56	663	21.6	231	2 PC4155	Ig gamma-2b chain
57	654	21.3	577	2 I50731	Ig heavy chain - n
58	650	21.2	214	2 PC4202	monoclonal antibod
59	620	20.2	509	2 S17597	Ig delta chain (WI
60	619.5	20.2	221	2 S49220	Ig gamma-1 chain -
61	606	19.7	504	2 S00390	Ig gamma chain (cl
62	588.5	19.2	568	2 A45804	Ig mu chain C regi
63	586	19.1	143	2 S23624	Ig heavy chain V r
64	571	18.6	152	2 S14236	Ig gamma-1 chain C
65	549	17.9	342	2 A46529	Ig gamma chain (S.
66	538	17.5	170	2 A35944	Ig gamma-2a chain
67	536.5	17.5	573	2 S12838	Ig mu chain precu
68	534.5	17.4	154	2 JN0698	interleukin 2 prec
69	509.5	16.6	448	2 S31186	Ig heavy chain C r
70	501	16.3	119	2 S31107	Ig heavy chain - h
71	501	16.3	138	2 S31666	Ig heavy chain V r
72	501	16.3	160	2 S05271	Ig epsilon chain C
73	492	16.0	428	1 EHHU	Ig gamma-1 chain C
74	490	16.0	97	2 S26652	Ig variable region
75	489.5	15.9	147	2 I37780	Ig heavy chain, se
76	487	15.9	580	2 A46538	Ig heavy chain V r
77	486	15.8	119	2 D36005	Ig epsilon chain C
78	486	15.8	429	1 EHRT	Ig epsilon-chain -
79	485.5	15.8	426	2 I36948	Ig epsilon-chain - h
80	484	15.8	119	2 S31108	Ig heavy chain - h
81	483	15.7	140	2 S31686	Ig heavy chain V r
82	482.5	15.7	140	2 S70442	Ig heavy chain pre
83	482.5	15.7	155	2 S33509	interleukin-2 - Mo
84	480	15.6	123	2 S31114	Ig heavy chain - h
85	479	15.6	125	2 S30531	Ig heavy chain V r
86	478.5	15.6	154	2 S16241	Ig heavy chain V r
87	477.5	15.5	124	2 S20782	interleukin-2 prec
88	477.5	15.5	128	2 S28790	Ig heavy chain V r
89	477	15.4	1005	2 T18537	Ig heavy chain - c
90	474	15.4	119	2 C36005	Ig heavy chain V r
91	474	15.4	135	2 S31598	Ig heavy chain V r
92	474	15.4	140	2 S31588	Ig heavy chain V r
93	473.5	15.4	120	2 S48798	Ig heavy chain V r
94	470.5	15.3	118	2 S31105	Ig heavy chain (su
95	470.5	15.3	135	2 I37778	Ig variable region
96	470	15.3	119	2 S36005	Ig heavy chain V r
97	469.5	15.3	120	2 S44111	Ig heavy chain V-D
98	469.5	15.3	433	2 S31436	Ig epsilon chain -
99	469	15.3	127	2 S38489	Ig heavy chain - h
100	469	15.3	149	2 S31391	interleukin-2 prec

## ALIGNMENTS

## RESULT 1

CHINA

IG gamma-1 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004  
C:Accession: A93433; S36863; B90563; A90564; B91668; A91723; A02146  
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982  
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.  
A:Reference number: A93433; MUID:82274238; PMID:6287432  
A:Accession: A93433  
A:Molecule type: DNA  
A:Residues: 1-330 <ELL>  
A:Cross-references: UNIPROT:P01857; EMBL:Z17370  
A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,  
R:Harris, L.J.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S33904  
A:Accession: S36861  
A:Molecule type: DNA  
A:Residues: 2-330 <HAR>  
A:Cross-references: EMBL:Z17370  
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaïdo, T.; Nakai, S.; Honjo, T.  
Cell 29, 671-679, 1982  
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a  
A:Reference number: S33887; MUID:83001943; PMID:6811139  
A:Accession: S33887  
A:Molecule type: DNA  
A:Residues: 88-113;235-330 <TAK>  
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, G.M.  
Biochemistry 9, 3161-3170, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen  
A:Reference number: A90563; MUID:71064024; PMID:5489771  
A:Contents: myeloma protein Eu  
A:Accession: B90563  
A:Molecule type: protein  
A:Residues: 1-96, 'R', 98-135 <CUN>  
A:Note: this sequence has the G1m(3) marker, 97-Arg  
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen  
A:Reference number: A90564; MUID:71064025; PMID:5530842  
A:Contents: Eu  
A:Accession: A90564  
A:Molecule type: protein  
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,  
A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met  
R:Ponstingl, H.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),  
igen Primärstruktur.  
A:Reference number: A91668; MUID:77070269; PMID:826475  
A:Contents: myeloma protein Nie  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'O', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 278,  
A:Note: this sequence has the G1m(17) and G1m(1) markers  
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A:Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL  
A:Reference number: A91723; MUID:83289131; PMID:6884994  
A:Contents: myeloma protein KOL; disulfide bonds  
A:Accession: A91723  
A:Molecule type: protein  
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH  
A:Note: this sequence has the G1m(3) and G1m(non-1) markers  
R:Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970

A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 53.18; Score 1630.5; DB 2; Length 377;  
Best Local Similarity 82.0%; Pred. No. 3e-84;  
Matches 309; Conservative 10; Mismatches 11; Indels 47; Gaps 1;

QY 120 ASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSVHTTTPAVLQSS 179  
DB 1 ASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSVHTTTPAVLQSS 60

QY 180 GLYSLSVVTVPSSSLGTQYICNVNKKPSNTKVDKKV----- 217  
DB 61 GLYSLSVVTVPSSSLGTQYICNVNKKPSNTKVDKKVELKTLPLGDTTHTTCRCPPEKSC 120

QY 218 -----EPKSCDKTHTCPCPAPPELLGGPSVFLPFPKPKDT 252  
DB 121 DTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKPKDT 180

QY 253 LMSRTPVETCVVVDVSHEDPEVKFNMYVDGVEVHNAKTPREEQYNSTVRVSVLTVLH 312  
DB 181 LMSRTPVETCVVVDVSHEDPEVKFNMYVDGVEVHNAKTPREEQYNSTVRVSVLTVLH 240

QY 313 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVK 372  
DB 241 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRBEEMTKNQVSLTCLVK 300

QY 373 GFYPDIAVWESNGQPPENNYKTPPVLDSDGFFLYSKLTVDKSRWQQGNVSCSVMHE 432  
DB 301 GFYPDIAVWESNGQPPENNYKTPPVLDSDGFFLYSKLTVDKSRWQQGNVSCSVMHE 360

QY 433 ALNHVYTKQSLSPGK 449  
DB 361 ALNHVYTKQSLSPGK 377

RESULT 3  
A60764  
Ig gamma-3 chain C region, form LAT - human  
C;Species: Homo sapiens (man)  
C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004  
C;Accession: A60764  
R;Huck, S.; Lefranc, M.P.  
Immunogenetics 30, 250-257, 1989  
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, bi, c3, c5, u) with an IGHG4 convert  
A;Reference number: A60764; MUID:90007613; PMID:2571587  
A;Accession: A60764  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-377 <HUC>  
A;Cross-references: UNIPROT:Q8N4Y9  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 53.0%; Score 1628.5; DB 2; Length 377;  
Best Local Similarity 82.0%; Pred. No. 3.9e-84;  
Matches 309; Conservative 10; Mismatches 11; Indels 47; Gaps 1;

QY 120 ASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSVHTTTPAVLQSS 179  
DB 1 ASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSVHTTTPAVLQSS 60

QY 180 GLYSLSVVTVPSSSLGTQYICNVNKKPSNTKVDKKV----- 217  
DB 61 GLYSLSVVTVPSSSLGTQYICNVNKKPSNTKVDKKVELKTLPLGDTTHTTCRCPPEKSC 120

QY 218 -----EPKSCDKTHTCPCPAPPELLGGPSVFLPFPKPKDT 252  
DB 121 DTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKPKDT 180

QY 253 LMSRTPVETCVVVDVSHEDPEVKFNMYVDGVEVHNAKTPREEQYNSTVRVSVLTVLH 312  
DB 181 LMSRTPVETCVVVDVSHEDPEVKFNMYVDGVEVHNAKTPREEQYNSTVRVSVLTVLH 240

QY 313 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVK 372  
DB 241 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRBEEMTKNQVSLTCLVK 300

QY 373 GFYPDIAVWESNGQPPENNYKTPPVLDSDGFFLYSKLTVDKSRWQQGNVSCSVMHE 432  
DB 301 GFYPDIAVWESNGQPPENNYKTPPVLDSDGFFLYSKLTVDKSRWQQGNVSCSVMHE 360

QY 433 ALNHVYTKQSLSPGK 449  
DB 361 ALNHVYTKQSLSPGK 377

RESULT 4  
G2HU  
Ig gamma-2 chain C region - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 09-Jul-2004  
C;Accession: A93906; A92809; A90752; A93132; A02148  
R;Ellison, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
A;Reference number: A93906; MUID:82197621; PMID:6804948  
A;Accession: A93906  
A;Molecule type: DNA  
A;Residues: 1-326 <SL>  
A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; P  
A;Note: Lys-326 is probably removed posttranslationally  
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f  
A;Reference number: A92809; MUID:81007873; PMID:6774012  
A;Contents: myeloma protein Til  
A;Accession: A92809  
A;Molecule type: protein  
A;Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>  
A;Note: Trp-156 is at or near the complement-binding site  
R;Connell, G.B.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A;Title: The amino acid sequences of the three heavy chain constant region domains of a  
A;Reference number: A90752; MUID:80001357; PMID:113060  
A;Contents: myeloma protein Zie  
A;Accession: A90752  
A;Molecule type: protein  
A;Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, '222', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-  
A;Note: this sequence has since been revised  
R;Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g  
A;Reference number: A93132; MUID:80114419; PMID:118920  
A;Contents: Zie  
A;Accession: A93132  
A;Molecule type: protein  
A;Residues: 238-275 <HOF>  
R;Hofmann, T.; Parr, D.M.  
Submitted to the Atlas, March 1980  
A;Reference number: A94591  
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidati  
ned  
R;Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.  
A;Reference number: A90253; MUID:72033500; PMID:4940472  
A;Contents: annotation; myeloma protein Sa, disulfide bonds  
R;Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A;Title: Structural studies of immunoglobulin G.  
A;Reference number: A93157; MUID:69064124; PMID:5782707











A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-140, 'C', 142-374 <KH2>  
A;Cross-references: EMBL:X81695  
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 46.5%; Score 1429; DB 2; Length 374;  
Best Local Similarity 62.1%; Pred. No. 5.7e-73;  
Matches 282; Conservative 23; Mismatches 45; Indels 104; Gaps 4;

QY 1 EVOLVESGGDFVQPGGSLRVSCAASGFAPSH--YAMSMVRQAPCKGLEWYAYISSGSGT 58  
DB 20 QITLKESGPTLVKPTQTTLTCTTSGFSLKSGVGVGWIQPPGQALEWALI-FWDDK 78  
QY 59 YYSVDSVKGRTTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLG---TYVFDMSGQCTLL 115  
DB 79 RYSPSLRTRLTITKDTSKNQVLTMTNVDPADTATYICGVSVGEGYGGQYRPHSGQGTIV 138  
QY 116 TVSSASTKGPSVFPPLAPSSTSGTGAALGCLVKDYFPPEVTVSMNSGALTSGVHTPPAV 175  
DB 139 TVSS----- 142  
QY 176 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKSTKVDKKVRPKSCDKTHTCCPCAPE 235  
DB 143 -----EPKSCDKTHTCCPCAPE 160  
QY 236 LGGPSVFLPPPKPOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPRE 295  
DB 161 LGGPSVFLPPPKPOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPRE 220  
QY 296 EQYNSTRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPP 355  
DB 221 EQYNSTRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPP 280  
QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVD 415  
DB 281 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVD 340  
QY 416 KSRWQGNVPSVCSVMHSHYHNTQKSLSPGK 449  
DB 341 KSRWQGNVPSVCSVMHSHYHNTQKSLSPGK 374

RESULT 12  
G2MS11  
IG gamma-2b chain - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1990 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C;Accession: S25057; A26235; A26232; A26233; A53598  
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
submitted to the EMBL Data Library, July 1992  
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m  
A;Reference number: S25057  
A;Accession: S25057  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-474 <FIS>  
A;Cross-references: UNIPROT:P01866; EMBL:X67210; MID:G54826; PIDN:CAA47649.1; PID:G54827  
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obara, M.; Honjo, T.  
Nature 283, 786-789, 1980  
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from h  
A;Reference number: A02157; MUID:80120716; PMID:6766534  
A;Contents: a allele  
A;Accession: A02157  
A;Molecule type: DNA  
A;Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>  
A;Cross-references: GB:J00461  
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
Science 206, 1299-1303, 1979  
A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea  
A;Reference number: A26235; MUID:80081501; PMID:117549  
A;Contents: MPC 11

A;Accession: A26235  
A;Molecule type: mRNA  
A;Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUL>  
A;Note: Lys-474 is probably removed posttranslationally  
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
Science 206, 1303-1306, 1979  
A;Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob  
A;Reference number: A26232; MUID:80081502; PMID:117549  
A;Accession: A26232  
A;Molecule type: DNA  
A;Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUL>  
R;Olio, R.; Rougeon, F.  
Nature 296, 761-763, 1982  
A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm  
A;Reference number: A26233; MUID:82173203; PMID:6803173  
A;Contents: b allele  
A;Accession: A26233  
A;Molecule type: DNA  
A;Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>  
A;Cross-references: GB:J00461  
R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahash  
J. Biol. Chem. 269, 12345-12350, 1994  
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
A;Reference number: A53598; MUID:94216359; PMID:7512967  
A;Accession: A53598  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 234-251 <KIM>  
C;Comment: The a allele sequence is shown.  
C;Genetics:  
A;Introns: 138/1; 236/1; 258/1; 368/1  
C;Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: alternative splicing; duplication; glycoprotein; heterotrimer; immunoglobul  
F;157-222/Domain: immunoglobulin homology <IM1>  
F;236-257/Region: hinge  
F;281-350/Domain: immunoglobulin homology <IM2>  
F;387-454/Domain: immunoglobulin homology <IM3>  
F;152/Disulfide bonds: interchain (to light chain) #status predicted  
F;164-220, 288-348, 394-452/Disulfide bonds: #status predicted  
F;247, 250, 253, 256/Disulfide bonds: interchain (to heavy chain) #status predicted  
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 45.3%; Score 1390; DB 1; Length 474;  
Best Local Similarity 56.6%; Pred. No. 1.2e-70;  
Matches 260; Conservative 72; Mismatches 113; Indels 14; Gaps 4;

QY 1 EVOLVESGGDFVQPGGSLRVSCAASGFAPSHYAMSMVRQAPCKGLEWYAYISSGSGTY 60  
DB 20 EVOLQSGPELVNPGASVKMSCKASGYFTITYVMHWVKQKPGQGLEWIGYINPNKDKTKP 79  
QY 61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTY----YFDSWGGQTLTV 117  
DB 80 NEKFKGKATLTSKSSNTAYMELSLTSDSAVYYCAR----DYDYDFWYWGQTLTV 135  
QY 118 SASTKGPSVFPPLAPSSTSGTGAALGCLVKDYFPPEVTVSMNSGALTSGVHTPPAVLQ 177  
DB 136 SAAKTPPSVPLAPCCGTTGSSVSGCLVKGYFPPEVTVSMNSGSLSSVHTLSQALL 195  
QY 178 SGLYSLSSVTVTPSSSLGTQTYICNVNHNKSPNTKVDKVPKSCDKT-HTCPP----- 230  
DB 196 QSGLYTMSSSVTPSPSTWPSQTVCVAHPASSTTVDKKLEPSPSTINPCPFCKECHK 255  
QY 231 CPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 290  
DB 256 CPAPNLEGGPSVFLPPPNIKDVLMTSLTPKVTCTVVDVSEDDPDVQISFMVNNVEVHTAQ 315  
QY 291 TKPREEQYNSTRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPREPQV 350  
DB 316 QTTHREDYNSTRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPREPQV 375  
QY 351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYS 410

Db 376 YLLPPAPQLSKVSLCLVGFNPGLISVWTSNGHTEENYKDTAPVLSDSGSYFIYS 435  
Qy 411 KLTVDKSRWQGNVFCSCVMHEALNHHYTKSLSLSPGK 449  
Db 436 KLNMTSKWEKTDSPFCNVRHEGLKNLYLKTTISRSPGK 474

RESULT 13  
S01321  
Ig gamma-2b chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 23-Jul-1999  
C:Accession: S01321  
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.  
Eur. J. Biochem. 176, 287-295, 1988  
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a  
A:Reference number: S01320; MUID: 88329081; PMID: 3138116  
A:Accession: S01321  
A:Molecule type: mRNA  
A:Residues: 1-475 <Del>  
A:CROSS-references: EMBL:X13188; NID:gs1780; PIDN:CAA31580.1; PID:gs1781  
A:Note: this sequence was determined from the differentiated gene  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>  
F:159-223/Domain: immunoglobulin homology <IMM>

Query Match 44.5%; Score 1367.5; DB 2; Length 475;  
Best Local Similarity 56.2%; Pred. No. 2.1e-69;  
Matches 257; Conservative 75; Mismatches 116; Indels 9; Gaps 4;

Qy 1 EVQLVESGGDFVPGGSLRVSQAASGAFSPSHYAMSWVRQAPGKGLHWAYISSGSGTYY 60  
Db 20 QVQLQSGAEALRPGASVKLSCKASGYTLTSYGISWVKRQTQGLEIGEIYVPGSGSYF 79

Qy 61 SDSVIGRTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK-LGTYYFDSWGQGLTLTVSS 119  
Db 80 NEKFKGKATLVDRKSSSTAYLHLSLSDSDSAVYFCAGPRQVGLLPFGYWGQGLTLVTASA 139

Qy 120 ASTKGPSVPLAPSSKSTSGGTAALCLVKDYFPPPTVTVSNWNSGALTSGVHTFPAVLQSS 179  
Db 140 AKTTPPSVPLAPGCGDTTGSSTVTLCLVKGFPPESVTVTVSNWNSGSLSSVHTFPAVLQ-S 198

Qy 180 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKT-HTCPP-----CP 232  
Db 199 GLYTWSSVTVPSSTWPSQTVCVAHPASSSTTVBKKLEPSGPTSTINPCPCKECHKCP 258

Qy 233 APPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 292  
Db 259 APNLEGGPSVFIFPPNRIKDVLMISLTPTKVTCTVVDVSEDDPDVQISWFNVNVFLTAQTQ 318

Qy 293 PREEQYNSTYRVVSVLTVLDHDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYT 352  
Db 319 THREEYNSTIRVVSALPTQHQDWMGSEKFKCKVNNKDLPAPIERTISKIGLVRAPOVIY 378

Qy 353 LPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFYLSKL 412  
Db 379 LSPPPQLSRKDVSLTCLAVGSPEDISVWTSNGHTEENYKDTAPVLSDSGSYFIYSKL 438

Qy 413 TVDKSRWQGNVFCSCVMHEALNHHYTKSLSLSPGK 449  
Db 439 NMKTSKWEKTDSPFCNVRHEGLKNLYLKTTISRSPGK 475

RESULT 14  
I47159  
Ig gamma 2a chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47159  
R:Kacekovic, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s  
A:Reference number: I47158; MUID: 95015845; PMID: 7930579  
A:Accession: I47159  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:CROSS-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124  
C:Genetics:  
A:Gene: Igg2a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 41.1%; Score 1263; DB 2; Length 328;  
Best Local Similarity 69.6%; Pred. No. 9.4e-64;  
Matches 231; Conservative 43; Mismatches 52; Indels 6; Gaps 2;

Qy 120 ASTKGPSVPLAPSSKSTSGGTAALCLVKDYFPPPTVTVSNWNSGALTSGVHTFPAVLQSS 179  
Db 1 APKTAPSVPLAPCSRDTSGFNVALGCLASSYFFPEPVTVTWNSGALSSGVHTFPPSVLQPS 60

Qy 180 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 239  
Db 61 GLYSLSMVTVPASLSKSYTCNVNHPATTTKVDKRVGTIKTKPPCPICAPCESP----G 116

Qy 240 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 299  
Db 117 PSVFIFFPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHTAQTTPKKEOFN 176

Qy 300 STYRVSVSLTVLDHDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYVTLPPSRDE 359  
Db 177 STYRVSVSLPTQHQDWMGSEKFKCKVNNKDLPAPIRTIISKAKGTREPQVYVTLPPHAE 236

Qy 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPVLDSDSGSFYLSKLTVDKS 417  
Db 237 LRSKVSITCLVIGFYPPDIDVWQNRQPSPEGNRYRTTPQDDVDGTYFLYSKFSVDKA 296

Qy 418 RWQGNVFCSCVMHEALNHHYTKSLSLSPGK 449  
Db 297 SWQGGIFQCAVMHEALNHHYTKSISKTGK 328

RESULT 15  
S1866  
Ig gamma-1 chain C region - synthetic  
C:Species: synthetic  
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C>Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C:Accession: S1866  
R:Filipula, D.  
submitted to the EMBL Data Library, February 1993  
A:Description: Screening method for protein-protein interactions of cloned gene products.  
A:Reference number: S1866  
A:Molecule type: mRNA  
A:Residues: 1-255 <Full>  
A:CROSS-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069  
C:Keywords: immunoglobulin  
F:1-22/Region: Escherichia coli outer membrane protein A precursor  
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 41.0%; Score 1260; DB 4; Length 255;  
Best Local Similarity 97.5%; Pred. No. 1e-63; Indels 0; Gaps 0;

Qy 211 TKVDKVEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSH 270  
Db 17 TVAQADVESKSDKTHTCPPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSH 76

Qy 271 EDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVSLTVLDHDLNGKEYKCKVSNKAL 330  
Db 77 EDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVSLTVLDHDLNGKEYKCKVSNKAL 136

Qy	331	PAPIEKTISKAKQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPE	390
Db	137	PAPIEKTISKAKQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPE	196
Qy	391	NNYKTPPVLDSDGSPFLYSKLTVDKSRWQGNVFCVMHEALHNHYTKSLSLSPGK	449
Db	197	NNYKTPPVLDSDGSPFLYSKLTVDKSRWQGNVFCVMHEALHNHYTKSLSLSPGK	255

Search completed: August 1, 2005, 09:18:43  
Job time : 33.9571 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:55 ; Search time 151.023 Seconds  
(without alignments)  
1973.408 Million cell updates/sec

Title: US-10-089-500-53

Perfect score: 3071

Sequence: 1 EVLVESGGDFVQGGSLRV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

Uniprot\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2223	72.4	470	2	Q6PJA4
2	2212	72.0	478	2	Q6PI81
3	2211.5	72.0	475	2	Q6MZQ6
4	2191.5	71.4	473	2	Q6MZV7
5	2188.5	71.3	475	2	Q6GMW7
6	2187	71.2	466	2	Q6IN78
7	2187	71.2	472	2	Q6N089
8	2184.5	71.1	544	2	Q6PJ95
9	2172	70.7	480	2	Q6N094
10	2159	70.3	466	2	Q6N096
11	2158	70.3	470	2	Q7Z3W1
12	2149.5	70.0	473	2	Q6P055
13	2134	69.5	482	2	Q7Z351
14	2105.5	68.6	481	2	Q6N097
15	2083.5	67.8	469	2	Q7Z7P5
16	2064	67.2	476	2	Q6GMX1
17	2062.5	67.2	475	2	Q6N095
18	2056.5	67.0	465	2	Q6GMX6
19	2045	66.6	464	2	Q6MZU6
20	2042	66.5	480	2	Q6PJF1
21	2041.5	66.5	465	2	Q6P6C4
22	1998.5	65.1	521	2	Q8N4Y9
23	1967	64.1	518	2	Q6N030
24	1955	63.7	493	2	Q68CN4
25	1945	63.3	417	2	Q6N093
26	1841	59.9	473	2	Q8TC63
27	1818	59.2	348	2	Q6PYX1
28	1812.5	59.0	476	2	Q6MZX7
29	1767	57.5	330	1	GC1_HUMAN
30	1622.5	52.8	509	2	Q8NF17
31	1604	52.2	326	1	GC2_HUMAN

32	1590.5	51.8	327	1	GC4_HUMAN	P01861	homo sapien
33	1538.5	50.1	471	2	Q66K04	Q66K04	mus musculus
34	1538.5	50.1	487	2	Q65ZL2	Q65ZL2	mus ep. fv/
35	1530	49.8	458	2	Q65ZQ1	Q65ZQ1	homo sapien
36	1524.5	49.6	354	2	Q86TT2	Q86TT2	homo sapien
37	1521.5	49.5	473	2	Q91Z05	Q91Z05	mus musculus
38	1499	48.8	464	2	Q6PIP8	Q6PIP8	mus musculus
39	1485.5	48.4	463	2	Q91LC4	Q91LC4	mus musculus
40	1477.5	48.1	473	2	Q9DBL4	Q9DBL4	mus musculus
41	1457	47.4	470	2	Q7TMK1	Q7TMK1	mus musculus
42	1452.5	47.3	465	2	Q6PUB2	Q6PUB2	mus musculus
43	1450	47.2	472	2	Q6PUA7	Q6PUA7	mus musculus
44	1436	46.8	464	2	Q6PF95	Q6PF95	mus musculus
45	1409	45.9	474	2	Q8R3H6	Q8R3H6	mus musculus
46	1366.5	41.2	337	2	Q95M34	Q95M34	equus caball
47	1264	40.1	679	2	Q96PQ8	Q96PQ8	homo sapien
48	1230.5	40.1	323	1	GC_RABIT	P01870	oryctolagus
49	1216.5	39.6	329	1	GC2_CAVPO	P01862	cavia porce
50	1156	37.6	290	1	GC3_HUMAN	P01860	homo sapien
51	1152	37.5	326	1	GC1_RAT	P20759	rattus norv
52	1146.5	37.3	333	1	GCB_RAT	P20761	rattus norv
53	1142	37.2	324	1	GC1_MOUSE	P01868	mus musculus
54	1141	37.2	329	1	GC3_MOUSE	P22436	mus musculus
55	1139	37.1	393	1	GC1M_MOUSE	P01869	mus musculus
56	1130	36.8	398	1	GC3M_MOUSE	P03987	mus musculus
57	1126	36.7	330	1	GCAB_MOUSE	P01863	mus musculus
58	1123.5	36.6	335	1	GCAB_MOUSE	P01864	mus musculus
59	1121	36.5	399	1	GCAM_MOUSE	P01865	mus musculus
60	1118.5	36.4	329	1	GCC_RAT	P20762	rattus norv
61	1112	36.2	322	1	GCA_RAT	P20760	rattus norv
62	1087	35.4	336	1	GCB_MOUSE	P01866	mus musculus
63	1082	35.2	405	1	GCBM_MOUSE	P01867	mus musculus
64	901	29.3	597	2	Q96BE9	Q96BE9	homo sapien
65	897.5	29.2	606	2	Q6GMV2	Q6GMV2	homo sapien
66	890	29.0	613	2	Q8WUK1	Q8WUK1	homo sapien
67	874.5	28.5	584	2	Q6INK3	Q6INK3	xenopus lae
68	841	27.4	585	2	Q6GFX4	Q6GFX4	xenopus lae
69	834.5	27.2	303	2	Q6KAM2	Q6KAM2	mus musculus
70	833	27.1	493	2	Q6GMX2	Q6GMX2	homo sapien
71	823.5	26.8	494	2	Q96K68	Q96K68	homo sapien
72	813	26.5	593	2	Q61NM5	Q61NM5	xenopus lae
73	812	26.4	487	2	Q99KA4	Q99KA4	mus musculus
74	812	26.4	614	2	Q6DDQ7	Q6DDQ7	xenopus lae
75	810	26.4	493	2	Q8NCL6	Q8NCL6	homo sapien
76	802	26.1	479	2	Q6MZV6	Q6MZV6	homo sapien
77	801	26.1	487	2	Q6ZVX0	Q6ZVX0	homo sapien
78	799	26.0	499	2	Q8NSK4	Q8NSK4	homo sapien
79	794.5	25.9	486	2	Q91Z07	Q91Z07	mus musculus
80	790	25.7	479	2	Q91WP5	Q91WP5	mus musculus
81	788	25.7	483	2	Q6MZB8	Q6MZB8	homo sapien
82	784	25.5	485	2	Q6PDB8	Q6PDB8	mus musculus
83	772.5	25.2	494	2	Q6ZM64	Q6ZM64	homo sapien
84	769	25.0	519	2	Q6N092	Q6N092	homo sapien
85	764	24.9	480	2	Q91XE1	Q91XE1	mus musculus
86	762.5	24.8	484	2	Q8VEA0	Q8VEA0	mus musculus
87	760	24.7	487	2	Q8OZ17	Q8OZ17	mus musculus
88	757	24.6	613	2	Q8VCX7	Q8VCX7	mus musculus
89	752.5	24.5	614	2	Q7TMT6	Q7TMT6	mus musculus
90	727	23.7	597	2	Q6GMX5	Q6GMX5	homo sapien
91	727	23.7	597	2	Q6N010	Q6N010	homo sapien
92	721	23.5	498	2	Q6N041	Q6N041	homo sapien
93	721	23.5	597	2	Q9BQB8	Q9BQB8	homo sapien
94	715.5	23.3	595	2	Q8WUX4	Q8WUX4	homo sapien
95	715.5	23.3	625	2	Q96AA6	Q96AA6	homo sapien
96	713.5	23.0	500	2	Q6N091	Q6N091	homo sapien
97	707.5	23.2	620	2	Q6BRV0	Q6BRV0	homo sapien
98	705	22.9	480	2	Q96EY0	Q96EY0	homo sapien
99	703.5	22.9	480	2	Q6P089	Q6P089	homo sapien
100	699	22.8	497	2	Q8WY24	Q8WY24	homo sapien

ALIGNMENTS

```

RESULT 1
Q6PJA4 ID Q6PJA4 PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshuyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -.
DR HSP; P01861; IADO.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 72.4%; Score 2223; DB 2; Length 470;
Best Local Similarity 93.1%; Pred. No. 1.8e-136;
Matches 420; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

QY 1 EVQLVESGGDVFQPGSLRVCAASGFAPFASHYAMSVROARPGKLEWYAYISGSGSTYY 60
DB 20 EVQLVESGGGLVQPGSLRLSCVSGFTFSYMSWVRQAPGKLEWANIYKQDSEKRY 79
QY 61 SDSVKGRFTISRDNSKNTLYLQWRSIRLARSADVFCYTRVRLGTY--YFDSWQGGTLLTVS 118
DB 80 VDSVKGRFTISRDNAKNSLYLQWNSIRLAREDAVYICARDGSSWYRDWDFPQCGTLTVTS 139
QY 119 SASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPPTVTSVNSGALTSGVHTFPAVLQS 178
DB 140 SASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPPTVTSVNSGALTSGVHTFPAVLQS 199

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QY 179 SGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKYDKKVEPKSCDKTHTCPPCPAPELIG 238
DB 200 SGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKYDKKVEPKSCDKTHTCPPCPAPELIG 259
QY 239 GPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 298
DB 260 GPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319
QY 299 NSTYRVVSVLTVLVHODWLNKGYKCKVSNKALPAPIETKTISKAKGQPREPQVYTLPPSRD 358
DB 320 NSTYRVVSVLTVLVHODWLNKGYKCKVSNKALPAPIETKTISKAKGQPREPQVYTLPPSRD 379
QY 359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLKTVDKSR 418
DB 380 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLKTVDKSR 439
QY 419 WQGNVFCVSCVNHAEALHNHYTQKSLSLSPGK 449
DB 440 WQGNVFCVSCVNHAEALHNHYTQKSLSLSPGK 470

RESULT 2
Q6PI81 ID Q6PI81 PRELIMINARY; PRT; 478 AA.
AC Q6PI81;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshuyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -.
DR HSP; P01861; IADO.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.

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DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 72.0%; Score 2212; DB 2; Length 478;
Best Local Similarity 91.3%; Pred. No. 9.5e-136;
Matches 419; Conservative 10; Mismatches 20; Indels 10; Gaps 2;

QY 1 EVOLVESGDFVPPGSLRVSCLASGFAFHYAMSWVRQAPGKLEWAVYISGGSGTYY 60
DB 20 EVOLVESGGLVPPGSLRVSCLASGFTFSYMSWVRQAPGKLEWAVIKDGSKYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTY-----VKLGTYFP--DSWG 110
DB 80 VDSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYICAREFESTMTTNADYYFFYMDVWG 139
QY 111 QGTLTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPPEPVTVSNNGALTSGVH 170
DB 140 KGTTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPPEPVTVSNNGALTSGVH 199
QY 171 TPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPP 230
DB 200 TPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPP 259
QY 231 CPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 290
DB 260 CPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 319
QY 291 TKPREEQNSTYRVSVLTVLHQDLNMGKEYCKKVSNNKALPAPIEKTISKAKGQPREPQV 350
DB 320 TKPREEQNSTYRVSVLTVLHQDLNMGKEYCKKVSNNKALPAPIEKTISKAKGQPREPQV 379
QY 351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFFLYS 410
DB 380 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFFLYS 439
QY 411 KLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 449
DB 440 KLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 478

RESULT 3
Q6MZQ6 PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686G11190.
GN Name=DKFZp686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640347; CAE45972.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.

DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 72.0%; Score 2211.5; DB 2; Length 475;
Best Local Similarity 91.2%; Pred. No. 1e-135;
Matches 416; Conservative 13; Mismatches 20; Indels 7; Gaps 1;

QY 1 EVOLVESGDFVPPGSLRVSCLASGFAFHYAMSWVRQAPGKLEWAVYISGGSGTYY 60
DB 20 EVOLVESGGLVPPGSLRVSCLASGFTFRYAMSWVRQAPGKLEWAVISGSSGVNTYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTY-----YFDSMQGT 113
DB 80 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYICARADYRDYQSPAYWYFDVWGRGT 139
QY 114 LITVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPPEPVTVSNNGALTSGVHTFP 173
DB 140 LVSVAASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPPEPVTVSNNGALTSGVHTFP 199
QY 174 AVLOSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCA 233
DB 200 AVLOSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCA 259
QY 234 PELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 293
DB 260 PELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319
QY 294 REEQNSTYRVSVLTVLHQDLNMGKEYCKKVSNNKALPAPIEKTISKAKGQPREPQVYTL 353
DB 320 REEQNSTYRVSVLTVLHQDLNMGKEYCKKVSNNKALPAPIEKTISKAKGQPREPQVYTL 379
QY 354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFFLYSKLT 413
DB 380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFFLYSKLT 439
QY 414 VDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 449
DB 440 VDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 475

RESULT 4
Q6MZV7 PRELIMINARY; PRT; 473 AA.
AC Q6MZV7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686C11235.
GN Name=DKFZp686C11235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RG The German Human cDNA Consortium;
RA Bloecker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAE45920.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
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DR SMART: SM00406; IGV: 1.
DR PROSITE; PS00335; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 9476EAB4C0BFC447 CRC64;

Query Match 71.4%; Score 2191.5; DB 2; Length 473;
Best Local Similarity 90.1%; Pred. No. 28-134;
Matches 409; Conservative 21; Mismatches 19; Indels 5; Gaps 1;

QY 1 EVQLVESGGDFVQPGGSLRVSQAAGSFAPSHYAMWVRQAPGKLEWYAYISSGSGSYTY 60
DB 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 ELQLVESGGGLVQPGGSLRLSCAASGFTFSFEMWVRQAPGKLEWLSYITRSNGTVY 79
QY 61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK-----LGTYY-FDSWGGTLL 115
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 ADSLQGRFTISRDNARNSLYLQWNSLRADTAAYVYCARQNEHTSPWYPSFFDYWGQGLV 139
QY 116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPEPTVSWNSGALTSGVHTFPAV 175
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
140 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFLEPPTVSWNSGALTSGVHTFPAV 199
QY 176 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPE 235
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
200 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPE 259
QY 236 LLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
260 LLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 319
QY 296 EGYNSTRYRVSVLTVLHQLDNLGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
320 EGYNSTRYRVSVLTVLHQLDNLGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 379
QY 356 SRDELTKQVSLTCLVKGYFIPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTV 415
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
380 SREEMTKQVSLTCLVKGYFIPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTV 439
QY 416 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
440 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 473

RESULT 5
Q6GMW7 PRELIMINARY; PRT; 475 AA.
ID Q6GMW7
AC Q6GMW7;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG.V.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;

Query Match 71.3%; Score 2188.5; DB 2; Length 475;
Best Local Similarity 91.0%; Pred. No. 3.2e-134;
Matches 415; Conservative 11; Mismatches 23; Indels 7; Gaps 2;

QY 1 EVQLVESGGDFVQPGGSLRVSQAAGSFAPSHYAMWVRQAPGKLEWYAYISSGSGSYTY 60
DB 20 EVQLVESGGGLVQPGGSLRLSCVASFYLSRHAHWVRQAPGKLEWYVSGISNSNSTY 79
QY 61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK-----LGTYY-FDSWGGT 113
DB 80 ADSVKGRFTISRDYKNTLYLQGLSLRAEDKAVYYCAPACRCGDTCLNFFYGLDVGWGGT 139
QY 114 LLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPEPTVSWNSGALTSGVHTFP 173
DB 140 TVIVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPEPTVSWNSGALTSGVHTFP 199
QY 174 AVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPA 233
DB 200 AVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPA 259
QY 234 PELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 293
DB 260 PELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319
QY 294 REEQYNSTRYRVSVLTVLHQLDNLGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 353
DB 320 REEQYNSTRYRVSVLTVLHQLDNLGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379
QY 354 PPSRDELTKQVSLTCLVKGYFIPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLT 413
DB 380 PPSRDELTKQVSLTCLVKGYFIPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLT 439
QY 414 VDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
DB 440 VDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 475

RESULT 6
Q6IN78 PRELIMINARY; PRT; 466 AA.
ID Q6IN78
AC Q6IN78;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
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[illegible]

Db	319	EQYNSTYRVVSVLTVTHQDNLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPVVTLPP	378
Qy	356	SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVD	415
Db	379	SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVD	438
Qy	416	KSRWQGNVFCFSVMHEALHNHYTQKSLSLSPGK	449
Db	439	KSRWQGNVFCFSVMHEALHNHYTQKSLSLSPGK	472
RESULT 8			
Q6FU95	ID	Q6FU95	PRELIMINARY; PRT; 544 AA.
AC	06PAJ95;		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Hypothetical protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Primary B-Cells;		
RC	MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,		
RA	Jones S.-J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Primary B-Cells;		
RC	Strausberg R.;		
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.		
RL	ENBL; BC019046; AAH19046.1; -.		
DR	HSSP; P01861; IADO.		
DR	InterPro; IPR003599; Ig.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003597; Ig.c1.		
DR	InterPro; IPR003006; Ig.MHC.		
DR	InterPro; IPR003596; Ig.V.		
DR	Pfam; PF07654; C1-set; 3.		
DR	SMART; SM00409; IG; 2.		
DR	SMART; SM00407; IGc1; 3.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS00835; IG LIKE; 4.		
DR	PROSITE; PS00290; IG MHC.		
KW	Hypothetical protein.		
SQ	SEQUENCE 544 AA; 60102 MW; 1895814B297C668 CRC64;		

Query Match 71.1%; Score 2184.5; DB 2; Length 544;  
Best Local Similarity 87.4%; Pred. No. 7e-134;  
Matches 418; Conservative 12; Mismatches 29; Indels 19; Gaps 2;

Qy	1	EVQLVESGGGVQPGGSLRLVCAASGFAFISHYAMSWVRQAQPKGLIEWWAYISGGSGGTTY	60
Db	20	QAQLVESGGGVQPGGSLRLSCAASGFRFSNYGMHWVRQAQPKGLIEWAVFYSDESKTY	79
Qy	61	SDSVKGRFTTISRDNSKNTLYIQMWSLRRAEDSAVYFCTRVKLCTY-----YFDSWGGQT	113
Db	80	AASVKGRFTTISRDNSKNTLSIQMWSLRVEDTAVYCAKQKPWYSNSWFLTNFDSWGRGT	139
Qy	114	LLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPPVTVVNSGALTSGVHTPP	173
Db	140	LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVVNSGALTSGVHTPP	199
Qy	174	AVLQSSGLYSISVVTVVPSSSLGQTQYICNVNHPKPSNTKDKVKPKSCDKKTHCTCPPCA	233
Db	200	AVLQSSGLYSLSVVTVVPSSSLGQTQYICNVNHPKPSNTKDKVKPKSCDKKTHCTCPPCA	259
Qy	234	PELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNNYVGDGEVFNHAKTKP	293
Db	260	PELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNNYVGDGEVFNHAKTKP	319
Qy	294	REQYNSTYRVVSVLTVLHQDLNMGKEYCKVKSNKALPAPIEKTISKAKGQPREPQVYTL	353
Db	320	REQYNSTYRVVSVLTVLHQDLNMGKEYCKVKSNKALPAPIEKTISKAKGQPREPQVYTL	379
Qy	354	PPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSKLT	413
Db	380	PPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSKLT	439
Qy	414	VDKSRWQGGNVFSCSVMEALHNHYTQKSLSLSPKAPTSSTKTKTQLEHLLDLQ	471
Db	440	VDKSRWQGGNVFSCSVMEALHNHYTQKSLSLSP-----ELQLEESCAEAQ	485

RESULT 9

Q6N094

ID

Q6N094

PRELIMINARY;

PRT;

480 AA.

AC

Q6N094

05-JUN-2004 (TrEMBLrel. 27, Created)

DT

05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT

05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE

Hypothetical protein DKFZp686O01196.

GN

Name=DKFZp686O01196;

OS

Homo sapiens (Human)

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

ON

NCBI\_TaxID=9606;

RX

[1]

RP

SEQUENCE FROM N.A.

RC

TISSUE=Human esophagus tumor;

RG

The German Human cDNA Consortium;

RA

Wambolt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

RA

Pobo G., Han M., Wiemann S.;

RL

Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

DR

EMBL; BX640622; CAE45776.1; -.

DR

HSSP; P01861; 1ADQ.

DR

InterPro; IPR003599; IG.

DR

InterPro; IPR007110; IG-like.

DR

InterPro; IPR003597; IG\_cl.

DR

InterPro; IPR003006; IG\_MHC.

DR

InterPro; IPR003596; IG\_v.

DR

Pfam; PF07654; Cl-set; 3.

DR

SMART; SM00409; IG; 2.

DR

SMART; SM00407; IGel; 3.

DR

SMART; SM00406; IGv; 1.

DR

PROSITE; PS50835; IG LIKE; 4.

DR

PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.

SW

Hypothetical protein.

Qy

SEQUENCE

480 AA; 52612 MW; 2252473D35AEC18 CRC64;

Query Match 70.7%; Score 2172; DB 2; Length 480;  
Best Local Similarity 88.1%; Pred. No. 3.8e-133;  
Matches 406; Conservative 21; Mismatches 22; Indels 12; Gaps 1;

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QY 1 EVOLVESGDFVQPGSLRVSCAASGPAFPAHYAMSVWRQAPGKLEWVAVISSGGSTYY 60
Db 20 EEELVESGGGLVQPGESLRSLSCAASGTFRFSFNNVWRQAPGKLEWVAVINSRNEKYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTYYTYPDSWCOGTLTVSSA 108
Db 80 GESVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTYYTYPDSWCOGTLTVSSA 139
QY 109 WGQGTLLTVSSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSG 168
Db 140 WGQGTLLTVSSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSG 199
QY 169 VHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTC 228
Db 200 VHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTC 259
QY 229 PPCPAPELLGSPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSG 288
Db 260 PPCPAPELLGSPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSG 319
QY 289 AKTPREEQNSTYRVSVTLVHQDLNGKEYCKVSNKALPAPIETISKAKGQPREP 348
Db 320 AKTPREEQNSTYRVSVTLVHQDLNGKEYCKVSNKALPAPIETISKAKGQPREP 379
QY 349 QVTVLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 408
Db 380 QVTVLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 439
QY 409 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
Db 440 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 480
```

```
RESULT 10
Q6N096 PRELIMINARY; PRT; 466 AA.
AC Q6N096;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKF2p686I15196.
GN Name=DKF2p686I15196;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640620; CAE45774.1; --
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 466 AA; 50926 MW; 01E91B748D6D57CA CRC64;
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Query Match 70.3%; Score 2159; DB 2; Length 466;  
Best Local Similarity 90.8%; Pred. No. 2.6e-132;  
Matches 407; Conservative 16; Mismatches 24; Indels 2; Gaps 1;

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QY 1 EVOLVESGDFVQPGSLRVSCAASGPAFPAHYAMSVWRQAPGKLEWVAVISSGGSTYY 60
Db 20 EEELVESGGGLVQPGESLRSLSCAASGTFRFSFNNVWRQAPGKLEWVAVINSRNEKYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTYYTYPDSWCOGTLTVSSA 120
Db 80 AEFVQGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTYYTYPDSWCOGTLTVSSA 137
QY 121 STKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180
Db 138 STKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 197
QY 181 LYSLSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPCPAPELLGGP 240
Db 198 LYSLSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPCPAPELLGGP 257
QY 241 SVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREBOYNS 300
Db 258 SVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREBOYNS 317
QY 301 TYRVSVTLVHQDLNGKEYCKVSNKALPAPIETISKAKGQPREPQVYITLPPSRDEL 360
Db 318 TYRVSVTLVHQDLNGKEYCKVSNKALPAPIETISKAKGQPREPQVYITLPPSRDEL 377
QY 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDSRWQ 420
Db 378 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDSRWQ 437
QY 421 QGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
Db 438 QGNVFCSCVMHEALHNHYTQKSLSLSPGK 466
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```
RESULT 11
Q7Z5W1 PRELIMINARY; PRT; 470 AA.
AC Q7Z5W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hoeh P.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2];
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
```

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RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAH53984.1; -.
DR HSSP; P01857; 1H2H.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_2.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 70.3%; Score 2158; DB 2; Length 470;
Best Local Similarity 90.1%; Pred. No. 3e-132;
Matches 409; Conservative 14; Mismatches 23; Indels 8; Gaps 3;

QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWYAYISSGSGGTYY 60
DB 20 EVQLVESGGGLVQPGGSLRLVSCVAGFTLNYYDMHVRQGIKGLGWVSKIGTAGD-RYY 78
QY 61 SDSVAGRFTISRDNSKNTLYLQMSLRADSDAVYFCTR-----VKLGTYVFDMSGQGTL 115
DB 79 AGSVAGRFTISRENKDSLYLQMSLRVGDAAVYICARGAGRWAPLGA--FDIWQGTWV 136
QY 116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
DB 137 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 196
QY 176 LOSGLYSLSSVTVVPSSSLGTQTYICNVNKKPSNTKVDKKVEPKSCDKTHTCPCPAPE 235
DB 197 LOSGLYSLSSVTVVPSSSLGTQTYICNVNKKPSNTKVDKKVEPKSCDKTHTCPCPAPE 256
QY 236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 295
DB 257 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 316
QY 296 EQYNSTYRVSVVLTVLHODWLNKGYCKVKSNKALPAPIEKTISKAKGPREPQVYTLPP 355
DB 317 EQYNSTYRVSVVLTVLHODWLNKGYCKVKSNKALPAPIEKTISKAKGPREPQVYTLPP 376
QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVD 415
DB 377 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVD 436
QY 416 KSRWQGNVFCSCVNHVHEALHNHYTKSLSPGK 449
DB 437 KSRWQGNVFCSCVNHVHEALHNHYTKSLSPGK 470

RESULT 12
Q6P055 PRELIMINARY; PRT; 473 AA.
AC Q6P055;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Moore S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore S.I., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC05820; AAH5820.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match 70.0%; Score 2149.5; DB 2; Length 473;
Best Local Similarity 89.6%; Pred. No. 1.e-131;
Matches 407; Conservative 12; Mismatches 30; Indels 5; Gaps 2;

QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWYAYISS--GGSGT 58
DB 20 EAHLVESGGGLVQPGGSLRLVSCGSGFTFSGAWLSWVRQAPGKGLEWYARIQTDDGGTT 79
QY 59 YYSVSVKGRFTISRDNSKNTLYLQMSLRADSDAVYFCTRVKLGTY---YFDSMGQGL 115
DB 80 HYGTAVKGRFTVSRDDSRNTLYLQMSLRDTEDTAFYCATGSMNTVGLTGPDSWGQGLTV 139
QY 116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
DB 140 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 199
QY 176 LOSGLYSLSSVTVVPSSSLGTQTYICNVNKKPSNTKVDKKVEPKSCDKTHTCPCPAPE 235
DB 200 LOSGLYSLSSVTVVPSSSLGTQTYICNVNKKPSNTKVDKKVEPKSCDKTHTCPCPAPE 259
QY 236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 295
DB 260 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 319
QY 296 EQYNSTYRVSVVLTVLHODWLNKGYCKVKSNKALPAPIEKTISKAKGPREPQVYTLPP 355
DB 320 EQYNSTYRVSVVLTVLHODWLNKGYCKVKSNKALPAPIEKTISKAKGPREPQVYTLPP 379
QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVD 415
DB 380 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVD 439
QY 416 KSRWQGNVFCSCVNHVHEALHNHYTKSLSPGK 449
DB 440 KSRWQGNVFCSCVNHVHEALHNHYTKSLSPGK 473

RESULT 13
```





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:10 ; Search time 32.5277 seconds  
(without alignment)  
1284.140 Million cell updates/sec

Title: US-10-089-500-54  
Perfect score: 568  
Sequence: 1 DIOWTQSPSLASVGRVT.....HQYSKLPWTFGQTKVEIKR 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_16Dec04:\*

1:	Geneseqp1980s:*
2:	Geneseqp1990s:*
3:	Geneseqp2000s:*
4:	Geneseqp2001s:*
5:	Geneseqp2002s:*
6:	Geneseqp2003as:*
7:	Geneseqp2003bs:*
8:	Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	568	100.0	108	4	AAB81988
2	568	100.0	128	4	AAB81999
3	562	98.9	108	6	ABU11011
4	561	98.8	128	4	AAB81994
5	555	97.7	128	4	AAB81997
6	551	97.0	128	4	AAB81993
7	548	96.5	108	4	AAB81986
8	545	96.0	128	4	AAB81995
9	545	96.0	128	4	AAB81996
10	544	95.8	128	4	AAB81998
11	532	93.7	128	4	AAB81992
12	514	90.5	108	4	AAB81990
13	514	90.5	108	6	ABU11013
14	514	90.5	128	3	AAB01628
15	514	90.5	128	4	AAB81978
16	514	90.5	128	6	ABU11003
17	513	90.3	128	2	AAR33257
18	507	89.3	110	2	AAR70673
19	507	89.3	110	5	ABP61242
20	507	89.3	237	2	AAW70703
21	507	89.3	650	5	ABP61241
22	506	89.1	128	2	AAW28368
23	505	88.9	107	2	AAW68805
24	505	88.9	107	2	AAW70625
25	505	88.9	107	5	ABP61194



99 480 84.5 246 8 ADH50846 Aah50846 SGIV RPB4  
100 480 84.5 256 3 AAY55072 Aay55072 Interleuk

## ALIGNMENTS

## RESULT 1

AAB81988  
ID AAB81988 standard; protein; 108 AA.  
XX  
AC AAB81988;  
XX  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 54.  
XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX  
OS Synthetic.  
XX  
PN WO200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
XX  
PR 30-SEP-1999; 99JP-00278291.  
PR 06-APR-2000; 2000JP-00105088.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
DR WPI; 2001-266143/27.  
XX

New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.

PS Claim 22; Page 172-173; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumors, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 568; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 1.3e-35;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60  
DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60  
QY 61 RFSGGSGTDYTLTISSLPEDIATYFCHQYSKLPWTFQGTQKVEIKR 108  
DB 61 RFSGGSGTDYTLTISSLPEDIATYFCHQYSKLPWTFQGTQKVEIKR 108

## RESULT 2

AAB81999  
ID AAB81999 standard; protein; 128 AA.

XX  
AC AAB81999;

XX  
DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein #8.  
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX  
OS Synthetic.  
XX  
PN WO200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
XX  
PR 30-SEP-1999; 99JP-00278291.  
PR 06-APR-2000; 2000JP-00105088.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
DR WPI; 2001-266143/27.  
DR N-PSDB; AAF86913.

XX New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX  
PS Example 1; Page 166; 183pp; Japanese.  
XX  
CC The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumors, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention

XX SQ Sequence 128 AA;

Query Match 100.0%; Score 568; DB 4; Length 128;  
Best Local Similarity 100.0%; Pred. No. 1.5e-35;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60  
DB 21 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 80  
QY 61 RFSGGSGTDYTLTISSLPEDIATYFCHQYSKLPWTFQGTQKVEIKR 108  
DB 81 RFSGGSGTDYTLTISSLPEDIATYFCHQYSKLPWTFQGTQKVEIKR 128

## RESULT 3

ABU11011  
ID ABU11011 standard; protein; 108 AA.

XX  
AC ABU11011;

XX  
DT 04-FEB-2003 (first entry)

XX Modified ganglioside GD3 antibody associated protein #4.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX  
OS Synthetic.

XX  
PN WO200278739-A1.

XX  
PD 10-OCT-2002.

XX  
PF 29-MAR-2002; 2002WO-JP003170.

XX  
PR 29-MAR-2001; 2001JP-00097483.



PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Shitara K, Niwa R, Kanazawa J, Aaada M;  
 XX WPI; 2003-067410/06.  
 XX  
 XX Drugs containing genetically-modified antibody against ganglioside GD3,  
 PT its fragment, immunocompetent cell activators or/and antitumor agents in  
 PT combination, applicable in treating malignant tumor like melanoma.  
 XX  
 XX Claim 8; Page 100; 121pp; Japanese.  
 XX  
 XX The invention describes drugs contain a genetically-modified antibody  
 CC against ganglioside GD3 or its fragment and at least 1 of a substance  
 CC capable of activating immunocompetent cells and a substance having an  
 CC antitumor activity in combination. The drugs can be used to treat tumour  
 CC like melanoma and can provide a treatment with enhanced therapeutic  
 CC effect and little side-reactions, particularly to relieve problems of  
 CC side-effects during the conventional single administration. This sequence  
 CC represents a protein associated with the anti- ganglioside GD3 antibody  
 XX  
 XX Sequence 108 AA;

Query Match 98.9%; Score 562; DB 6; Length 108;  
 Best Local Similarity 99.1%; Pred. No. 3.6e-35;  
 Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAVKLLIFYSNHLHSGVPS 60  
 DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAPKLLIFYSNHLHSGVPS 60  
 QY 61 RFSGGSGTDYTLTISSLPEDYATYFCHQYSKLPMTFGGQTKVEIKR 108  
 DB 61 RFSGGSGTDYTLTISSLPEDYATYFCHQYSKLPMTFGGQTKVEIKR 108

RESULT 4  
 AAB81994  
 ID AAB81994 standard; protein; 128 AA.  
 XX  
 XX AAB81994;  
 XX  
 XX 03-JUL-2001 (first entry)  
 XX  
 XX Ganglioside GD3 specific antibody related protein #3.  
 XX  
 XX Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 XX Cancer.  
 XX  
 XX Synthetic.  
 XX  
 XX WO200123432-A1.  
 XX  
 XX 05-APR-2001.  
 XX  
 XX 29-SEP-2000; 2000WO-JP006774.  
 XX  
 XX 30-SEP-1999; 99JP-00278291.  
 XX  
 XX 06-APR-2000; 2000JP-00105088.  
 XX  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 XX Hanai N, Shitara K, Nakamura K, Niwa R;  
 XX  
 XX WPI; 2001-266143/27.  
 XX  
 XX N-PSDB; AAF86898.  
 XX  
 XX New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.  
 XX  
 XX Example 1; Page 155-156; 183pp; Japanese.

XX  
 CC The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumors, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention  
 XX  
 XX Sequence 128 AA;  
 Query Match 98.8%; Score 561; DB 4; Length 128;  
 Best Local Similarity 98.1%; Pred. No. 5e-35;  
 Matches 106; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAVKLLIFYSNHLHSGVPS 60  
 DB 21 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAVKLLIFYSNHLHSGVPS 80  
 QY 61 RFSGGSGTDYTLTISSLPEDYATYFCHQYSKLPMTFGGQTKVEIKR 108  
 DB 81 RFSGGSGTDYTLTISSLPEDYATYFCHQYSKLPMTFGGQTKVEIKR 128

RESULT 5  
 AAB81997  
 ID AAB81997 standard; protein; 128 AA.  
 XX  
 XX AAB81997;  
 XX  
 XX 03-JUL-2001 (first entry)  
 XX  
 XX Ganglioside GD3 specific antibody related protein #6.  
 XX  
 XX Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 XX cancer.  
 XX  
 XX Synthetic.  
 XX  
 XX WO200123432-A1.  
 XX  
 XX 05-APR-2001.  
 XX  
 XX 29-SEP-2000; 2000WO-JP006774.  
 XX  
 XX 30-SEP-1999; 99JP-00278291.  
 XX  
 XX 06-APR-2000; 2000JP-00105088.  
 XX  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 XX Hanai N, Shitara K, Nakamura K, Niwa R;  
 XX  
 XX WPI; 2001-266143/27.  
 XX  
 XX N-PSDB; AAF86907.  
 XX  
 XX New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.  
 XX  
 XX Example 1; Page 161-162; 183pp; Japanese.

XX  
 CC The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumors, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention  
 XX  
 XX Sequence 128 AA;  
 Query Match 97.7%; Score 555; DB 4; Length 128;  
 Best Local Similarity 98.1%; Pred. No. 1.4e-34;  
 Matches 106; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAVKLLIFYSNHLHSGVPS 60

```
Db      21 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNWKQKPKAPKLLIFYSNLSHGVP 80
Qy      61 RFSGGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFQGGTKVEIKR 108
Db      81 RFSGGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFQGGTKVEIKR 128

RESULT 6
AAB81993
ID AAB81993 standard; protein; 128 AA.
XX
AC AAB81993;
XX
DT 03-JUL-2001 (first entry)
DE Ganglioside GD3 specific antibody related protein #2.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 153; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;

Query Match          97.0%; Score 551; DB 4; Length 128;
Best Local Similarity 97.2%; Pred. No. 2.8e-34;
Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNWKQKPKAPKLLIFYSNLSHGVP 60
Db      21 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNWKQKPKAPKLLIFYSNLSHGVP 80
Qy      61 RFSGGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFQGGTKVEIKR 108
Db      81 RFSGGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFQGGTKVEIKR 128

RESULT 7
AAB81986
ID AAB81986 standard; protein; 108 AA.
XX
AC AAB81986;
XX
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```
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 10.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 143-144; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 108 AA;

Query Match          96.5%; Score 548; DB 4; Length 108;
Best Local Similarity 96.3%; Pred. No. 4.1e-34;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNWKQKPKAPKLLIFYSNLSHGVP 60
Db      1 DIQMTQSPSSLSASVGDRVTITCSASQDISNVLNWKQKPKAPKLLIFYSNLSHGVP 60
Qy      61 RFSGGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFQGGTKVEIKR 108
Db      61 RFSGGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFQGGTKVEIKR 108

RESULT 8
AAB81995
ID AAB81995 standard; protein; 128 AA.
XX
AC AAB81995;
XX
DT 03-JUL-2001 (first entry)
DE Ganglioside GD3 specific antibody related protein #4.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
```

PR 30-SEP-1999; 99JP-00278291.  
PR 06-APR-2000; 2000JP-00105088.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX Hanai N, Shitara K, Nakamura K, Niwa R;  
XX WPI; 2001-266143/27.  
DR N-PSDB; AAF86901.  
XX New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX  
XX Example 1; Page 157-158; 183pp; Japanese.  
PS  
XX The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumours, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX  
XX Sequence 128 AA;  
Query Match 96.0%; Score 545; DB 4; Length 128;  
Best Local Similarity 95.4%; Pred. No. 8e-34;  
Matches 103; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 1 DIQWTQSPSSLSASVGRVITTCASQDISNLYNWYQOKPKDKAVKLLIFYSSNLHSGVPS 60  
DB 21 DIQWTQSPSSLSASVGRVITTCASQDISNLYNWYQOKPKDKAVKLLIFYSSNLHSGVPS 80  
QY 61 RFSGGSGTDYTLTISLQPEDIATYFCHQYSKLPWTFGGGTKEIKR 108  
DB 81 RFSGGSGTDYTLTISLQPEDIATYFCHQYSKLPWTFGGGTKEIKR 128  
RESULT 9  
AAB81996  
ID AAB81996 standard; protein; 128 AA.  
XX  
XX AAB81996;  
XX 03-JUL-2001 (first entry)  
XX Ganglioside GD3 specific antibody related protein #5.  
DE Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
OS Synthetic.  
XX WO200123432-A1.  
XX  
XX 05-APR-2001.  
XX 29-SEP-2000; 2000WO-JP006774.  
XX 30-SEP-1999; 99JP-00278291.  
XX 06-APR-2000; 2000JP-00105088.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX Hanai N, Shitara K, Nakamura K, Niwa R;  
XX WPI; 2001-266143/27.  
XX N-PSDB; AAF86904.  
XX New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.

XX Example 1; Page 159-160; 183pp; Japanese.  
XX The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumours, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX  
XX Sequence 128 AA;  
Query Match 96.0%; Score 545; DB 4; Length 128;  
Best Local Similarity 95.4%; Pred. No. 8e-34;  
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 DIQWTQSPSSLSASVGRVITTCASQDISNLYNWYQOKPKDKAVKLLIFYSSNLHSGVPS 60  
DB 21 DIQWTQSPSSLSASVGRVITTCASQDISNLYNWYQOKPKDKAVKLLIFYSSNLHSGVPS 80  
QY 61 RFSGGSGTDYTLTISLQPEDIATYFCHQYSKLPWTFGGGTKEIKR 108  
DB 81 RFSGGSGTDYTLTISLQPEDIATYFCHQYSKLPWTFGGGTKEIKR 128  
RESULT 10  
AAB81998  
ID AAB81998 standard; protein; 128 AA.  
XX  
XX AAB81998;  
XX 03-JUL-2001 (first entry)  
XX Ganglioside GD3 specific antibody related protein #7.  
DE Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
OS Synthetic.  
XX WO200123432-A1.  
XX  
XX 05-APR-2001.  
XX 29-SEP-2000; 2000WO-JP006774.  
XX 30-SEP-1999; 99JP-00278291.  
XX 06-APR-2000; 2000JP-00105088.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX Hanai N, Shitara K, Nakamura K, Niwa R;  
XX WPI; 2001-266143/27.  
XX N-PSDB; AAF86912.  
XX New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX  
XX Example 3; Page 164-165; 183pp; Japanese.  
PS  
XX The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumours, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX  
XX Sequence 128 AA;  
Query Match 95.8%; Score 544; DB 4; Length 128;  
Best Local Similarity 96.3%; Pred. No. 9.5e-34;  
Matches 104; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNLSHGVPVS 60
DB 21 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNLSHGVPVS 80
QY 61 RFSGGSGGTDYTLTITSSLOPEDFATYFCHQYSKLPWTFGQGTKEIKR 108
DB 81 RFSGGSGGTDYTLTITSSLOPEDFATYFCHQYSKLPWTFGQGTKEIKR 128

RESULT 11
AAB81992
ID AAB81992 standard; protein; 128 AA.
XX
AC AAB81992;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #1.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PN New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 1; Page 150-151; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;

Query Match 93.7%; Score 532; DB 4; Length 128;
Best Local Similarity 93.5%; Pred. No. 7.7e-33;
Matches 101; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNLSHGVPVS 60
DB 21 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNLSHGVPVS 80
QY 61 RFSGGSGGTDYTLTITSSLOPEDFATYFCHQYSKLPWTFGQGTKEIKR 108
DB 81 RFSGGSGGTDYTLTITSSLOPEDFATYFCHQYSKLPWTFGQGTKEIKR 128

RESULT 12
AAB81990
ID AAB81990 standard; protein; 108 AA.
XX
XX
XX
```

```
AC AAB81990;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 56.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX
OS Mus musculus.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PN New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 11; Page 174-175; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 108 AA;

Query Match 90.5%; Score 514; DB 4; Length 108;
Best Local Similarity 88.9%; Pred. No. 1.5e-31;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNLSHGVPVS 60
DB 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNLSHGVPVS 60
QY 61 RFSGGSGGTDYTLTITSSLOPEDFATYFCHQYSKLPWTFGQGTKEIKR 108
DB 61 RFSGGSGGTDYTLTITSSLOPEDFATYFCHQYSKLPWTFGQGTKEIKR 108

RESULT 13
AABU1013
ID AABU1013 standard; protein; 108 AA.
XX
AC AABU1013;
XX
DT 04-FEB-2003 (first entry)
XX
DE Modified ganglioside GD3 antibody associated protein #6.
XX
KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
OS Mus musculus.
XX
PN WO200278739-A1.
XX
PD 10-OCT-2002.
XX
PF 29-NAR-2002; 2002WO-JP003170.
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XX PR 29-MAR-2001; 2001JP-00097483.
XX XX
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PI Shitara K, Niwa R, Kanazawa J, Asada M;
XX PR WPI; 2003-067410/06.
XX XX
XX PR Drugs containing genetically-modified antibody against ganglioside GD3,
XX PT its fragment, immunocompetent cell activators or/and antitumor agents in
XX PT combination, applicable in treating malignant tumor like melanoma.
XX XX
XX PS Claim 7; Page 113; 121pp; Japanese.
XX CC
XX CC The invention describes drugs contain a genetically-modified antibody
XX CC against ganglioside GD3 or its fragment and at least 1 of a substance
XX CC capable of activating immunocompetent cells and a substance having an
XX CC antitumor activity in combination. The drugs can be used to treat tumour
XX CC like melanoma and can provide a treatment with enhanced therapeutic
XX CC effect and little side-reactions, particularly to relieve problems of
XX CC side-effects during the conventional single administration. This sequence
XX CC represents a protein associated with the anti- ganglioside GD3 antibody
XX XX
XX SQ Sequence 108 AA;
Query Match 90.5%; Score 514; DB 6; Length 108;
Best Local Similarity .88.9%; Pred. No. 1.5e-31;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIQWTQSPSSLSASVGRVITTCASQDISNLYLNWYQOKPKAVKLLIFYSSNLHSGVPS 60
DB 1 DIQWTQSPSSLSASVGRVITTCASQDISNLYLNWYQOKPKAVKLLIFYSSNLHSGVPS 60
QY 61 RFSGGSGTDYTLTISLQPEDATYFCHQYSKLPWTFGGTKVEIKR 108
DB 61 RFSGGSGTDYTLTISLQPEDATYFCHQYSKLPWTFGGTKVEIKR 108
RESULT 14
AAB01628
ID AAB01628 standard; protein; 128 AA.
AC AAB01628;
XX XX
XX DT 07-DEC-2000 (first entry)
XX DE Murine immunoglobulin light chain variable region.
XX XX
XX KW Mouse; immunoglobulin; L chain; light chain; variable region; cancer;
XX KW humanised antibody.
XX OS Mus sp.
XX XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..20
XX FT /label= signal_peptide
XX FT Protein 21..128
XX FT /label= mature_immunoglobulin_light_chain_v_region
XX XX
XX PN EP1013761-A2.
XX XX
XX PD 28-JUN-2000.
XX XX
XX PF 18-SEP-1992; 99EP-00124345.
XX XX
XX PR 18-SEP-1991; 91JP-00238375.
XX PR 18-SEP-1992; 92EP-00116026.
XX XX
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX XX
XX PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
XX XX
```

```
DR WPI; 2000-402204/35.
DR N-PSDB; AAA51004.
XX XX
XX PT New humanized chimera antibody KM-871 useful for treating cancer,
XX PT comprises variable region of mouse monoclonal antibody, reactive with
XX PT ganglioside and human antibody constant region.
XX PS
XX PS Claim 14; Page 28-29; 65pp; English.
XX XX
XX CC The present sequence is a murine immunoglobulin light chain variable
XX CC region from plasmid KM-641. The coding sequence was used in the creation
XX CC of an expression vector, along with the sequence for a human antibody, to
XX CC produce humanised chimaeric antibodies, which can be used to treat
XX CC cancer. Humanised chimaeric antibodies are more effective than mouse
XX CC antibodies as they do not provoke a reaction in the human and side
XX CC effects, such as the formation of anti-mouse immunoglobulin antibody and
XX CC the rapid half-life of the immunoglobulins, do not occur
XX XX
XX SQ Sequence 128 AA;
Query Match 90.5%; Score 514; DB 3; Length 128;
Best Local Similarity 88.9%; Pred. No. 1.8e-31;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIQWTQSPSSLSASVGRVITTCASQDISNLYLNWYQOKPKAVKLLIFYSSNLHSGVPS 60
DB 21 DIQWTQSPSSLSASVGRVITTCASQDISNLYLNWYQOKPKAVKLLIFYSSNLHSGVPS 80
QY 61 RFSGGSGTDYTLTISLQPEDATYFCHQYSKLPWTFGGTKVEIKR 108
DB 81 RFSGGSGTDYTLTISLQPEDATYFCHQYSKLPWTFGGTKVEIKR 128
RESULT 15
AAB81978
ID AAB81978 standard; protein; 128 AA.
XX XX
XX AC AAB81978;
XX XX
XX DT 03-JUL-2001 (first entry)
XX DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 2.
XX XX
XX KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX KW cancer.
XX OS Mus musculus.
XX XX
XX PN WO200123432-A1.
XX XX
XX PD 05-APR-2001.
XX XX
XX PF 29-SEP-2000; 2000WO-JP006774.
XX XX
XX PR 30-SEP-1999; 99JP-00278291.
XX PR 06-APR-2000; 2000JP-00105088.
XX XX
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX XX
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX XX
XX DR WPI; 2001-266143/27.
XX XX
XX PT New human type complementation-determining region-transplanted antibody
XX PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX PT of e.g. tumors, with low antigenicity, little side effects but potent
XX PT activity in cancer.
XX XX
XX PS Example 1; Page 140; 183pp; Japanese.
XX XX
XX CC The present invention describes a monoclonal antibody which can react
XX CC specifically with ganglioside GD3. The antibody and its derivatives are
XX CC useful in the diagnosis and therapy of tumours, particularly cancer
```

CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention

CC of the invention

XX

Sequence 128 AA;

Query Match 90.5%; Score 514; DB 4; Length 128;  
Best Local Similarity 88.9%; Pred. No. 1.8e-31;  
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPKDKAVKLLIFYSSNLHSGVPS 60

Db 21 DIQMTQASSLPALGDRVTWSCASQDISYLNWYQKPDGTVKLLIFYSNLHSGVPS 80

QY 61 RFSGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108

Db 81 RFSGGSGTDYSLTISNLEPEDATYFCHOYSKLPWTFGGTKLEIKR 128

Search completed: August 1, 2005, 09:10:09  
Job time : 33.5277 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:59:16 ; Search time 8.19913 Seconds  
(without alignments)  
983.287 Million cell updates/sec

Title: US-10-089-500-54

Perfect score: 568

Sequence: 1 D1QMTQSPSLSASVGRVT.....HOYSLKLPWTFGQTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfilese1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	514	90.5	128	4	US-09-225-322B-10
2	514	90.5	128	4	US-09-225-322B-19
3	514	90.5	128	4	US-09-764-304-10
4	514	90.5	128	4	US-09-764-304-19
5	507	89.3	491	4	US-10-011-125A-2
6	503	88.6	110	4	US-09-440-781-94
7	491	86.4	108	3	US-09-065-059-3
8	487	85.7	127	3	US-08-649-100-33
9	484	85.2	214	1	US-08-458-516-12
10	481	84.7	110	4	US-09-440-781-95
11	480	84.5	107	2	US-07-934-373C-17
12	480	84.5	107	2	US-08-652-558-2
13	480	84.5	107	3	US-08-437-642B-17
14	480	84.5	107	4	US-08-146-206C-17
15	480	84.5	107	4	US-09-705-686-17
16	480	84.5	107	4	US-09-705-392A-17
17	480	84.5	107	4	US-09-705-398-17
18	480	84.5	107	5	PCT-US93-07832-17
19	480	84.5	109	3	US-07-934-373C-47
20	480	84.5	109	3	US-08-437-642B-47
21	480	84.5	214	2	US-07-934-373C-40
22	480	84.5	214	2	US-08-788-800-11
23	480	84.5	214	3	US-08-437-642B-40
24	480	84.5	214	3	US-09-097-309-2
25	480	84.5	214	3	US-09-097-171A-2
26	480	84.5	214	3	US-09-460-587-2
27	480	84.5	214	4	US-09-940-166A-2
28	480	84.5	214	5	PCT-US93-07832-40
29	480	84.5	233	2	US-07-934-373C-25
30	480	84.5	233	3	US-08-437-642B-25
31	480	84.5	233	4	US-08-146-206C-25
32	480	84.5	233	4	US-09-705-686-25
33	480	84.5	233	4	US-09-705-392A-25
34	480	84.5	233	4	US-09-705-398-25
35	480	84.5	233	5	PCT-US93-07832-25
36	480	84.5	237	3	US-09-097-309-6
37	480	84.5	237	3	US-09-097-171A-10
38	480	84.5	237	3	US-09-422-712B-2
39	480	84.5	237	3	US-09-607-756-2
40	480	84.5	237	3	US-09-460-587-6
41	480	84.5	237	1	US-08-940-166A-6
42	479	84.3	107	1	US-08-458-516-8
43	476	83.8	107	3	US-09-254-189-1
44	475	83.6	108	3	US-08-974-899-3
45	475	83.6	108	4	US-09-795-798-3
46	475	83.6	111	1	US-08-137-117D-67
47	475	83.6	111	2	US-08-436-717-67
48	475	83.6	126	1	US-08-137-117D-71
49	475	83.6	126	2	US-08-436-717-71
50	472	83.1	214	2	US-07-934-373C-39
51	472	83.1	214	3	US-08-437-642B-39
52	472	83.1	214	5	PCT-US93-07832-39
53	470	82.7	107	2	US-07-934-373C-18
54	470	82.7	107	3	US-08-437-642B-18
55	470	82.7	107	4	US-08-146-206C-18
56	470	82.7	107	4	US-09-648-067A-14
57	470	82.7	107	4	US-09-705-686-18
58	470	82.7	107	4	US-09-705-392A-18
59	470	82.7	107	4	US-09-705-398-18
60	470	82.7	107	5	PCT-US93-07832-18
61	468	82.4	107	2	US-08-652-558-35
62	466	82.0	109	2	US-07-934-373C-3
63	466	82.0	109	3	US-08-437-642B-3
64	466	82.0	109	4	US-08-146-206C-3
65	466	82.0	109	4	US-09-705-686-3
66	466	82.0	109	4	US-09-705-392A-3
67	466	82.0	109	4	US-09-705-398-3
68	466	82.0	109	5	PCT-US93-07832-3
69	465	81.9	105	3	US-09-199-149-31
70	465	81.9	212	4	US-10-011-125A-5
71	464	81.7	109	4	US-09-386-658A-4
72	463	81.5	109	4	US-09-802-083-4
73	462	81.3	107	2	US-08-318-157B-6
74	462	81.3	107	4	US-09-253-794-6
75	462	81.3	109	3	US-09-157-370-3
76	461	81.2	131	1	US-08-236-520-2
77	461	81.2	131	2	PCT-US95-05262-2
78	460	81.1	114	2	US-08-561-521-43
79	460	81.1	114	5	PCT-US95-01219-43
80	458	80.6	127	4	US-09-809-733-10
81	457	80.5	112	3	US-08-487-761-13
82	456	80.3	102	3	US-09-199-149-10
83	456	80.3	102	3	US-09-199-149-29
84	456	80.3	108	2	US-08-070-116A-7
85	456	80.3	108	2	US-08-116-247-9
86	456	80.3	108	3	US-09-199-149-14
87	456	80.3	108	4	US-08-557-050-7
88	456	80.3	108	4	US-08-454-899G-100
89	456	80.3	108	4	US-09-348-224-9
90	455	80.1	108	3	US-09-025-769B-14
91	455	80.1	108	4	US-09-490-070A-14
92	455	80.1	108	4	US-09-490-153-14
93	455	80.1	108	4	US-09-490-324-14
94	453	79.8	108	2	US-08-602-725-29
95	453	79.8	108	3	US-09-199-149-7
96	452	79.6	107	1	US-08-458-516-9
97	452	79.6	107	2	US-08-561-521-6
98	452	79.6	107	2	US-08-652-558-34
99	452	79.6	107	3	US-09-025-203-15
100	452	79.6	107	4	US-09-999-021-15

## ALIGNMENTS

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RESULT 1
US-09-225-322B-10
; Sequence 10, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
US-09-225-322B-19
Query Match 90.5%; Score 514; DB 4; Length 128;
Best Local Similarity 88.9%; Pred. No. 1.3e-43;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNVLNYYQKPKDKAVKLLIFYSNLSHGVP 60
DB 21 DIQMTQATASSLPASLGDRVTISCSASQDISNVLNYYQKPKDGTVKLLIFYSNLSHGVP 80
QY 61 RFGSGSGTDTLTITSSLPEDIAFYFCHQYSKLPWTFGGKVEIKR 108
DB 81 RFGSGSGTDTLTITSSLPEDIAFYFCHQYSKLPWTFGGKVEIKR 128

RESULT 2
US-09-764-304-10
; Sequence 10, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cdNA KM-641
US-09-764-304-10
Query Match 90.5%; Score 514; DB 4; Length 128;
Best Local Similarity 88.9%; Pred. No. 1.3e-43;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNVLNYYQKPKDKAVKLLIFYSNLSHGVP 60
DB 21 DIQMTQATASSLPASLGDRVTISCSASQDISNVLNYYQKPKDGTVKLLIFYSNLSHGVP 80
QY 61 RFGSGSGTDTLTITSSLPEDIAFYFCHQYSKLPWTFGGKVEIKR 108
DB 81 RFGSGSGTDTLTITSSLPEDIAFYFCHQYSKLPWTFGGKVEIKR 128

RESULT 2
US-09-225-322B-19
; Sequence 19, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
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RESULT 7
US-09-065-059-3
; Sequence 3, Application US/09065059
; Patent No. 6068841
; GENERAL INFORMATION:
; APPLICANT: SEINO, Ken-ichiro
; APPLICANT: KAYAGAKI, No. 6068841uhiko
; APPLICANT: YAGITA, Hideo
; APPLICANT: OKUMURA, Ko
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDermott, Will & Emery
; STREET: 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,059
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Bucca Ph.D., Daniel
; REGISTRATION NUMBER: P-42,368
; REFERENCE/DOCKET NUMBER: P-42,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-518-5100
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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US-09-065-059-3
Query Match 86.4%; Score 491; DB 3; Length 108;
Best Local Similarity 84.3%; Pred. No. 2e-41;
Matches 91; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLSHGVPVS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLSHGVPVS 60

QY 61 RPSGGSGTDYTLTISSLPEDIAFYCHQYSKLPWTFCQGTKEIKR 108
Db 61 RPSGGSGTDYTLTISSLPEDIAFYCHQYSEFPWTFCQGTKEIKR 108

RESULT 8
US-08-649-100-33
; Sequence 33, Application US/08649100
; Patent No. 6114507
; GENERAL INFORMATION:
; APPLICANT: SHIRAKAWA, KAMON
; APPLICANT: MATSUE, TOMOKAZU
; APPLICANT: NAGATA, SHIGEKAZU
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
; TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,100
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-458-516-12
Query Match 85.2%; Score 484; DB 1; Length 214;
Best Local Similarity 83.3%; Pred. No. 2.2e-40;
Matches 90; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLSHGVPVS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLSHGVPVS 60

QY 61 RPSGGSGTDYTLTISSLPEDIAFYCHQYSKLPWTFCQGTKEIKR 108
Db 61 RPSGGSGTDYTLTISSLPEDIAFYCHQYSEFPWTFCQGTKEIKR 108

;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-649-100-33
Query Match 85.7%; Score 487; DB 3; Length 127;
Best Local Similarity 86.0%; Pred. No. 6.1e-41;
Matches 92; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLSHGVPVS 60
Db 21 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLSHGVPVS 80

QY 61 RPSGGSGTDYTLTISSLPEDIAFYCHQYSKLPWTFCQGTKEIKR 107
Db 81 RPSGGSGTDYTLTISSLPEDIAFYCHQYSEFPWTFCQGTKEIKR 127

RESULT 9
US-08-458-516-12
; Sequence 12, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIb/IIIa
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-458-516-12
Query Match 85.2%; Score 484; DB 1; Length 214;
Best Local Similarity 83.3%; Pred. No. 2.2e-40;
Matches 90; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLSHGVPVS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLSHGVPVS 60

QY 61 RPSGGSGTDYTLTISSLPEDIAFYCHQYSKLPWTFCQGTKEIKR 108
Db 61 RPSGGSGTDYTLTISSLPEDIAFYCHQYSEFPWTFCQGTKEIKR 108
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Db 61 RFGSGSGDTYLTITSSLPDPDPATYFCQQGNTLPWTFGGQTKVEIKR 108

RESULT 10

US-09-440-781-95  
; Sequence 95, Application US/09440781  
; Patent No. 6632326  
; GENERAL INFORMATION:  
; APPLICANT: Yvonne Man-ye Chen et al.  
; TITLE OF INVENTION: ANTIBODY VARIANTS  
; FILE REFERENCE: P1469R1  
; CURRENT APPLICATION NUMBER: US/09/440,781  
; CURRENT FILING DATE: 1999-11-16  
; NUMBER OF SEQ ID NOS: 99  
; SEQ ID NO 95  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: artificial  
; LOCATION: 1-110  
; OTHER INFORMATION: humanized antibody light chain variable domain  
US-09-440-781-95

Query Match 84.7%; Score 481; DB 4; Length 110;  
Best Local Similarity 81.5%; Pred. No. 2e-40;  
Matches 88; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNNLHSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRANEQLSNLYLNWYQOKPKDKAVKLLIFYSNNLHSGVPS 60

Qy 61 RFGSGSGDTYLTITSSLPDPDPATYFCQQGNTLPWTFGGQTKVEIKR 108

Db 61 RFGSGSGDTYLTITSSLPDPDPATYFCQQGNTLPWTFGGQTKVEIKR 108

RESULT 11

US-07-934-373C-17  
; Sequence 17, Application US/07934373C  
; Patent No. 5821337  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/934,373C  
; FILING DATE: 21-Aug-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P2  
; TELECOMMUNICATION INFORMATION:

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNNLHSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRANEQLSNLYLNWYQOKPKDKAVKLLIFYSNNLHSGVPS 60

; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-07-934-373C-17

Query Match 84.5%; Score 480; DB 2; Length 107;  
Best Local Similarity 86.0%; Pred. No. 2.5e-40;  
Matches 92; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNNLHSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQDIRNYLNWYQOKPKDKAVKLLIFYSNNLHSGVPS 60

Qy 61 RFGSGSGDTYLTITSSLPDPDPATYFCQQGNTLPWTFGGQTKVEIK 107

Db 61 RFGSGSGDTYLTITSSLPDPDPATYFCQQGNTLPWTFGGQTKVEIK 107

RESULT 12

US-08-652-558-2  
; Sequence 2, Application US/08652558  
; Patent No. 5861155  
; GENERAL INFORMATION:  
; APPLICANT: LIN, AUGUSTINE YEE-THARN  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER & WITCOFF  
; STREET: 75 STATE STREET, 23RD FLOOR  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02109

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,558  
; FILING DATE: JUNE 6, 1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/IB94/00387  
; FILING DATE: NOVEMBER 21, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YANKWICH, LEON R.  
; REGISTRATION NUMBER: 30,237  
; REFERENCE/DOCKET NUMBER: 95,497-L  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-345-9100  
; TELEFAX: 617-345-9111  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-652-558-2

Query Match 84.5%; Score 480; DB 2; Length 107;  
Best Local Similarity 86.8%; Pred. No. 2.5e-40;  
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNNLHSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRANEQLSNLYLNWYQOKPKDKAVKLLIFYSNNLHSGVPS 60

QY 61 RFSGSGGTDYTLTISLQPEDIATYFCHQYKLPWTFQGTKEIK 106  
DB 61 RFSGSGGTDYTLTISLQPEDIATYFCHQYKLPWTFQGTKEIK 106

## RESULT 13

US-08-437-642B-17  
; Sequence 17, Application US/08437642B  
; Patent No. 6054297  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/437,642B  
; FILING DATE: 09-May-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/934373  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/146206  
; FILING DATE: 17-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992

; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P2C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

US-08-437-642B-17

Query Match 84.5%; Score 480; DB 3; Length 107;  
Best Local Similarity 86.0%; Pred. No. 2.5e-40;  
Matches 92; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

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DB 1 DIQMTQSPSSLSASVGRVTITCSAQDISNYLNWYQOKPKAVKLLIFYSSNLHSGVPS 60

QY 61 RFSGSGGTDYTLTISLQPEDIATYFCHQYKLPWTFQGTKEIK 107  
DB 61 RFSGSGGTDYTLTISLQPEDIATYFCHQYKLPWTFQGTKEIK 107

## RESULT 14

US-08-146-206C-17  
; Sequence 17, Application US/08146206C  
; Patent No. 6407213

; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; TITLE OF INVENTION: Method for Making Humanized Antibodies  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
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; FILING DATE: 17-No. 6407213-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

US-08-146-206C-17

Query Match 84.5%; Score 480; DB 4; Length 107;  
Best Local Similarity 86.0%; Pred. No. 2.5e-40;  
Matches 92; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

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DB 1 DIQMTQSPSSLSASVGRVTITCSAQDISNYLNWYQOKPKAVKLLIFYSSNLHSGVPS 60

QY 61 RFSGSGGTDYTLTISLQPEDIATYFCHQYKLPWTFQGTKEIK 107  
DB 61 RFSGSGGTDYTLTISLQPEDIATYFCHQYKLPWTFQGTKEIK 107

## RESULT 15

US-09-705-686-17  
; Sequence 17, Application US/09705686  
; Patent No. 6639055  
; GENERAL INFORMATION:

; APPLICANT: Carter, Paul J.  
; TITLE OF INVENTION: Method for Making Humanized Antibodies  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/705.686
; FILING DATE: 02-Nov-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
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Query Match      84.5%; Score 480; DB 4; Length 107;
Best Local Similarity 86.0%; Pred. No. 2.5e-40;
Matches 92; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

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Qy 61 RPSGGSGTDYTLTITSSLPEDPATYFCHQYSKLPMTFGQGTKVEIK 107
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Db 61 RPSGGSGTDYTLTITSSLPEDPATYFCHQYSKLPMTFGQGTKVEIK 107
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

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Title: US-10-089-500-54

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Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	507	89.3	110	9	US-09-056-1608-103
8	507	89.3	110	14	US-10-234-671-101
9	507	89.3	110	17	US-10-974-591-101
10	507	89.3	237	9	US-09-056-1608-100
11	507	89.3	237	14	US-10-234-671-100
12	507	89.3	237	17	US-10-974-591-100
13	507	89.3	491	13	US-10-011-125-2
14	507	88.9	107	9	US-09-056-1608-15
15	505	88.9	107	14	US-10-234-671-15
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31	503	88.6	110	17	US-10-683-043-1
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93 481 84.7 110 14 US-10-234-671-109 Sequence 109, App  
94 481 84.7 110 14 US-10-234-671-111 Sequence 111, App  
95 481 84.7 110 14 US-10-234-671-113 Sequence 113, App  
96 481 84.7 110 15 US-10-624-153-95 Sequence 95, Appli  
97 481 84.7 110 17 US-10-683-043-2 Sequence 2, Appli  
98 481 84.7 110 17 US-10-683-043-3 Sequence 3, Appli  
99 481 84.7 110 17 US-10-683-043-4 Sequence 4, Appli  
100 481 84.7 110 17 US-10-683-043-6 Sequence 6, Appli

## ALIGNMENTS

RESULT 1  
US-09-764-304-10  
; Sequence 10, Application US/09764304  
; Patent No. US20020026036A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIIISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/764,304  
; EARLIER FILING DATE: 2001-01-19  
; EARLIER APPLICATION NUMBER: 09/225,322  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER APPLICATION NUMBER: US 08/454,680  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER APPLICATION NUMBER: US 08/408,133  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER APPLICATION NUMBER: US 08/292,178  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: light chain  
; OTHER INFORMATION: variable region  
US-09-764-304-19

Query Match 90.5%; Score 514; DB 9; Length 128;  
Best Local Similarity 88.9%; Pred. No. 7e-37;  
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNWYQOKPDKAVKLLIFYSSNLHSGVPS 60  
Db 21 DIQMTQTASSLPASLGRVTITCSASQDISNLYNWYQOKPDGTVKLLIFYSSNLHSGVPS 80  
Qy 61 RFSGGSGTDYTLTISSLPEDVATYFCHQYSKLPWTFGQGTKEIKR 108  
Db 81 RFSGGSGTDYSLTISNLEPEDVATYFCHQYSKLPWTFGGKLEIKR 128

RESULT 3  
US-10-265-713-10  
; Sequence 10, Application US/10265713  
; Publication No. US20030095964A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIIISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/10/265,713  
; EARLIER FILING DATE: 2002-10-08  
; EARLIER APPLICATION NUMBER: US/09/225,322  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER APPLICATION NUMBER: US 08/454,680  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER APPLICATION NUMBER: US 08/408,133  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER APPLICATION NUMBER: US 08/292,178  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; EARLIER FILING DATE: 1991-09-18

Query Match 90.5%; Score 514; DB 9; Length 128;  
Best Local Similarity 88.9%; Pred. No. 7e-37;  
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNWYQOKPDKAVKLLIFYSSNLHSGVPS 60  
Db 21 DIQMTQTASSLPASLGRVTITCSASQDISNLYNWYQOKPDGTVKLLIFYSSNLHSGVPS 80  
Qy 61 RFSGGSGTDYTLTISSLPEDVATYFCHQYSKLPWTFGQGTKEIKR 108  
Db 81 RFSGGSGTDYSLTISNLEPEDVATYFCHQYSKLPWTFGGKLEIKR 128

RESULT 2  
US-09-764-304-19  
; Sequence 19, Application US/09764304



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; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cdna KM-641
US-10-265-713-10

Query Match          90.5%; Score 514; DB 14; Length 128;
Best Local Similarity 88.9%; Pred. No. 7e-37; 5; Indels 0; Gaps 0;
Matches 96; Conservative 7; Mismatches 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSSNLHSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 DIQMTQTASSLPASLGRVITSCASQDISNYLNWYQKPKDGTGTVKLLIFYSSNLHSGVPS 80
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 RPSGGSGTDYTLTISLQPEDIATYFCHQYSKLPWTFFGGTKVEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 RPSGGSGTDYSLTISNLEPDIATYFCHQYSKLPWTFFGGTKLEIKR 128
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
US-10-265-713-19
; Sequence 19, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: light chain
US-10-265-713-19

Query Match          90.5%; Score 514; DB 14; Length 128;
Best Local Similarity 88.9%; Pred. No. 7e-37; 5; Indels 0; Gaps 0;
Matches 96; Conservative 7; Mismatches 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSSNLHSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 DIQMTQTASSLPASLGRVITSCASQDISNYLNWYQKPKDGTGTVKLLIFYSSNLHSGVPS 80
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 RPSGGSGTDYTLTISLQPEDIATYFCHQYSKLPWTFFGGTKVEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 RPSGGSGTDYSLTISNLEPDIATYFCHQYSKLPWTFFGGTKLEIKR 128
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

RESULT 5
US-10-166-626-10
; Sequence 10, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cdna KM-641
US-10-166-626-10

Query Match          90.5%; Score 514; DB 14; Length 128;
Best Local Similarity 88.9%; Pred. No. 7e-37; 5; Indels 0; Gaps 0;
Matches 96; Conservative 7; Mismatches 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSSNLHSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 DIQMTQTASSLPASLGRVITSCASQDISNYLNWYQKPKDGTGTVKLLIFYSSNLHSGVPS 80
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 RPSGGSGTDYTLTISLQPEDIATYFCHQYSKLPWTFFGGTKVEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 RPSGGSGTDYSLTISNLEPDIATYFCHQYSKLPWTFFGGTKLEIKR 128
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
US-10-166-626-19
; Sequence 19, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: variable region
US-10-166-626-19

```



## RESULT 9

US-10-974-591-101  
 ; Sequence 101, Application US/10974591  
 ; Publication No. US20050112126A1  
 ; GENERAL INFORMATION:

APPLICANT: Baca, Manuel  
 ; Wells, James A.  
 ; Presta, Leonard G.  
 ; Lowman, Henry B.  
 ; Chen, Yvonne M.

## TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/974,591

FILING DATE: 26-Oct-2004

CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/723752

FILING DATE: 27-NOV-2000

APPLICATION NUMBER: 08/908469

FILING DATE: 06-AUG-1997

APPLICATION NUMBER: 08/833504

FILING DATE: 07-APR-1997

## ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093P1D1C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 101:

SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 101:

US-10-974-591-101

Query Match

Best Local Similarity 89.3%; Score 507; DB 17; Length 110;

Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAVKLLIFVSSNLHSGVPS 60

DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAVKLLIFVSSNLHSGVPS 60

QY 61 RFGSGSGGTDYTLTISSLOPEDIATVFCQYSKLPMTFGGTVKVEIKR 108

DB 61 RFGSGSGGTDYTLTISSLOPEDIATVFCQYSKLPMTFGGTVKVEIKR 108

RESULT 10

US-09-056-160B-100

; Sequence 100, Application US/09056160B

; Patent No. US20020032315A1

; GENERAL INFORMATION:

APPLICANT: Baca, Manuel

; Wells, James A.

; Presta, Leonard G.

; Lowman, Henry B.

; Chen, Yvonne M.

; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

APPLICANT: Chen, Yvonne M.  
 ; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
 ; NUMBER OF SEQUENCES: 131  
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,160B

FILING DATE: 06-Apr-1998

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/054,856

FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hasek, Janet E.

REGISTRATION NUMBER: 28,616

REFERENCE/DOCKET NUMBER: P1093R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1896

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 100:

SEQUENCE CHARACTERISTICS:

LENGTH: 237 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-056-160B-100

Query Match

Best Local Similarity 89.3%; Score 507; DB 9; Length 237;

Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAVKLLIFVSSNLHSGVPS 60

DB 24 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAVKLLIFVSSNLHSGVPS 83

QY 61 RFGSGSGGTDYTLTISSLOPEDIATVFCQYSKLPMTFGGTVKVEIKR 108

DB 84 RFGSGSGGTDYTLTISSLOPEDIATVFCQYSKLPMTFGGTVKVEIKR 131

RESULT 11

US-10-234-671-100

; Sequence 100, Application US/10234671

; Publication No. US20030190317A1

; GENERAL INFORMATION:

APPLICANT: Baca, Manuel

; Wells, James A.

; Presta, Leonard G.

; Lowman, Henry B.

; Chen, Yvonne M.

; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/056160
; FILING DATE: 06-APR-1998
; APPLICATION NUMBER: 60/126446
; FILING DATE: 07-APR-1997
; APPLICATION NUMBER: 60/054856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093R2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-234-671-100

Query Match      89.3%; Score 507; DB 14; Length 237;
Best Local Similarity 88.0%; Pred. No. 5.2e-36;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPKAVKLLIFYSNLSHGVPVS 60
Db 24 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPKAPKLLIYFTSSLHSGVPVS 83
QY 61 RFSGSGSGTDYTLTISSLPEDIAIFYCHOYSKLPWTFGQGTKEIKR 108
Db 84 RFSGSGSGTDYTLTISSLPEDFATYYCQYSTVPTWTFGGTKVEIKR 131

RESULT 12
US-10-974-591-100
; Sequence 100, Application US/10974591
; Publication No. US2005012126A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/974,591
; FILING DATE: 26-Oct-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/723752
; FILING DATE: 27-NOV-2000
; APPLICATION NUMBER: 08/908469
; FILING DATE: 06-AUG-1997
; APPLICATION NUMBER: 08/833504

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/056160
; FILING DATE: 06-APR-1998
; APPLICATION NUMBER: 60/126446
; FILING DATE: 07-APR-1997
; APPLICATION NUMBER: 60/054856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093R2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-234-671-100

Query Match      89.3%; Score 507; DB 14; Length 237;
Best Local Similarity 88.0%; Pred. No. 5.2e-36;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPKAVKLLIFYSNLSHGVPVS 60
Db 24 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPKAPKLLIYFTSSLHSGVPVS 83
QY 61 RFSGSGSGTDYTLTISSLPEDIAIFYCHOYSKLPWTFGQGTKEIKR 108
Db 84 RFSGSGSGTDYTLTISSLPEDFATYYCQYSTVPTWTFGGTKVEIKR 131

RESULT 13
US-10-011-125-2
; Sequence 2, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-10-011-125-2

Query Match      89.3%; Score 507; DB 13; Length 491;
Best Local Similarity 88.0%; Pred. No. 1.1e-35;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPKAVKLLIFYSNLSHGVPVS 60
Db 24 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPKAPKLLIYFTSSLHSGVPVS 83
QY 61 RFSGSGSGTDYTLTISSLPEDIAIFYCHOYSKLPWTFGQGTKEIKR 108
Db 84 RFSGSGSGTDYTLTISSLPEDFATYYCQYSTVPTWTFGGTKVEIKR 131

RESULT 14
US-09-056-160B-15
; Sequence 15, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
```

;; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
;; NUMBER OF SEQUENCES: 131  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Genentech, Inc.  
;; STREET: 1 DNA Way  
;; CITY: South San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94080  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WinPatIn (Genentech)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/056,160B  
;; FILING DATE: 06-APR-1998  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 60/054,856  
;; FILING DATE: 06-AUG-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Haseak, Janet B.  
;; REGISTRATION NUMBER: 28,616  
;; REFERENCE/DOCKET NUMBER: P1093R2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650/225-1896  
;; TELEFAX: 650/952-9881  
;; INFORMATION FOR SEQ ID NO: 15:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 107 amino acids  
;; TYPE: Amino Acid  
;; TOPOLOGY: Linear  
US-09-056-160B-15

Query Match 88.9%; Score 505; DB 9; Length 107;  
Best Local Similarity 88.8%; Pred. No. 3.5e-36;  
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAVKLLIFYSSNLHSGVPS 60  
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAVKLLIFYTSSLHSGVPS 60  
Qy 61 RFSGGSGTDYTLTISSLPQEDPATYFCHQYKLPWTFGGTKVEIK 107  
Db 61 RFSGGSGTDYTLTISSLPQEDPATYFCHQYKLPWTFGGTKVEIK 107

RESULT 15  
US-10-234-671-15  
; Sequence 15, Application US/10234671  
; Publication No. US20030190317A1  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; Wells, James A.  
; Presta, Leonard G.  
; Lowman, Henry B.  
; Chen, Yvonne M.  
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/234,671  
;; FILING DATE: 03-Sep-2002  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/056160  
;; FILING DATE: 06-APR-1998  
;; APPLICATION NUMBER: 60/126446  
;; FILING DATE: 07-APR-1997  
;; APPLICATION NUMBER: 60/054856  
;; FILING DATE: 06-AUG-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Cui, Steven X.  
;; REGISTRATION NUMBER: 44,637  
;; REFERENCE/DOCKET NUMBER: P1093R2C1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650/225-8674  
;; TELEFAX: 650/952-9881  
;; INFORMATION FOR SEQ ID NO: 15:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 107 amino acids  
;; TYPE: Amino Acid  
;; TOPOLOGY: Linear  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-10-234-671-15  
Query Match 88.9%; Score 505; DB 14; Length 107;  
Best Local Similarity 88.8%; Pred. No. 3.5e-36;  
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAVKLLIFYSSNLHSGVPS 60  
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDKAVKLLIFYTSSLHSGVPS 60  
Qy 61 RFSGGSGTDYTLTISSLPQEDPATYFCHQYKLPWTFGGTKVEIK 107  
Db 61 RFSGGSGTDYTLTISSLPQEDPATYFCHQYKLPWTFGGTKVEIK 107  
Search completed: August 1, 2005, 09:28:02  
Job time : 28.4953 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 1, 2005, 08:58:15 ; Search time 6.11574 Seconds  
(without alignments)  
1699.125 Million cell updates/sec

Title: US-10-089-500-54

Perfect score: 568

Sequence: 1 DIQMTQSPSSLSASVGRVT.....HOYSKLPWTFGQGTQKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	480	84.5	108	1 K1HUAU	Ig kappa chain V-I
2	479	84.3	111	2 A38740	Ig kappa chain V r
3	477	84.0	111	2 E38740	Ig kappa chain V r
4	472	83.1	111	2 C38740	Ig kappa chain V r
5	469	82.6	111	2 C38740	Ig kappa chain V r
6	466	82.0	107	2 B49026	Ig kappa chain V r
7	462	81.3	127	2 S40367	Ig kappa chain V-J
8	461	81.2	108	1 KVM573	Ig kappa chain V r
9	461	81.2	108	2 S69900	Ig kappa chain (cl)
10	456	80.3	108	1 K1HURE	Ig kappa chain V-I
11	454	79.9	122	2 A29380	Ig kappa chain pre
12	452	79.6	108	2 S69903	Ig kappa chain (cl)
13	452	79.6	115	2 J10080	Ig kappa chain pre
14	451	79.4	129	2 S52789	Ig kappa chain V r
15	450	79.2	110	2 S44118	Ig kappa chain V-J
16	448	78.9	108	1 KVM5AR	Ig kappa chain V r
17	447	78.7	108	2 S69902	Ig kappa chain (cl)
18	447	78.7	109	2 PH0888	Ig kappa chain V r
19	447	78.7	126	2 A34904	Ig kappa chain pre
20	445	78.3	108	1 K1HUNG	Ig kappa chain V-I
21	445	78.3	108	2 I39154	Ig kappa chain (BR)
22	444	78.3	125	2 S40333	Ig kappa chain V-J
23	444	78.2	128	2 A26406	Ig kappa chain (cl)
24	443.5	78.1	107	2 S69901	Ig kappa chain (cl)
25	443	78.0	139	2 S40365	Ig kappa chain - h
26	442	77.8	133	2 S40331	Ig kappa chain - h
27	442	77.8	131	2 S40352	Ig kappa chain V-J
28	441.5	77.7	108	2 S38862	Ig kappa chain V r
29	441	77.6	108	2 B49047	Ig kappa chain V r

30	440	77.5	107	2 A48677	Ig kappa chain V-J
31	439	77.3	108	2 S44122	Ig kappa chain V r
32	439	77.3	108	2 C26405	Ig kappa chain V r
33	438	77.1	108	1 K1HURY	Ig kappa chain V-I
34	438	77.1	108	2 K19570	Ig kappa chain V r
35	437.5	77.0	107	2 S36275	Ig lambda chain V
36	437	76.9	107	2 B48677	Ig kappa chain V-J
37	437	76.9	107	2 B28044	Ig kappa chain V r
38	436	76.8	108	2 PL0282	Ig kappa chain V r
39	435	76.6	109	2 S31998	Ig kappa chain - h
40	434	76.4	107	2 S36264	Ig lambda chain V
41	434	76.4	107	2 A28044	Ig kappa chain V r
42	433	76.2	107	2 D48677	Ig kappa chain V-J
43	433	76.2	108	1 K1HUME	Ig kappa chain V-I
44	433	76.2	108	2 B26405	Ig kappa chain V r
45	433	76.2	127	2 PH1224	Ig kappa chain pre
46	431	75.9	129	2 S40369	Ig kappa chain - h
47	430.5	75.8	107	2 S69906	Ig kappa chain (cl)
48	429	75.5	108	1 K1HULY	Ig kappa chain V-I
49	429	75.5	108	2 S19674	Ig kappa chain V r
50	429	75.5	109	2 S31981	Ig kappa chain - h
51	429	75.5	141	2 A49134	Ig kappa chain V-I
52	427	75.2	107	2 S32188	Ig kappa chain V r
53	426.5	75.1	124	2 S40336	Ig kappa chain V-J
54	425	74.8	105	2 PH0087	Ig kappa chain V r
55	425	74.8	135	2 S24320	Ig kappa chain pre
56	424	74.6	107	2 I69017	Ig kappa chain V-I
57	424	74.6	108	1 K1HUUH	Ig kappa chain V-I
58	423.5	74.6	106	2 PC2397	anti-tetanus toxin
59	423	74.5	108	2 B30551	Ig kappa chain V r
60	423	74.5	108	2 S11124	Ig kappa chain V r
61	422	74.3	126	2 S40335	Ig kappa chain V-J
62	422	74.3	129	1 K1HUMK	Ig kappa chain pre
63	421	74.1	107	2 C48677	Ig light chain V-J
64	421	74.1	117	2 S46371	Ig kappa chain V-J
65	420	73.9	107	2 J10139	Ig kappa chain V r
66	420	73.9	108	1 K1HUKA	Ig kappa chain V-I
67	420	73.9	108	1 K1HUSW	Ig kappa chain V-I
68	420	73.9	125	2 S40349	Ig kappa chain V-J
69	419.5	73.9	125	2 S40315	Ig kappa chain - h
70	419	73.8	108	1 K1HUBN	Ig kappa chain V-I
71	419	73.8	122	2 S40370	Ig kappa chain - h
72	419	73.8	129	2 S52793	Ig kappa chain V r
73	419	73.8	132	2 S40334	Ig kappa chain - h
74	418	73.6	108	1 K1HUKU	Ig kappa chain V-I
75	418	73.6	108	2 S47182	Ig kappa chain - h
76	418	73.6	117	2 S46376	Ig kappa chain V-J
77	418	73.6	117	2 S42263	Ig kappa chain V r
78	418	73.6	117	2 S43528	Ig kappa chain V r
79	418	73.6	122	2 S40314	Ig kappa chain - h
80	417	73.4	108	1 K1HUBI	Ig kappa chain V-I
81	417	73.4	129	2 S40317	Ig kappa chain - h
82	416	73.2	108	1 K1HOUU	Ig kappa chain V-I
83	416	73.2	120	2 S46370	Ig kappa chain V-J
84	416	73.2	129	2 S52792	Ig kappa chain V r
85	416	73.2	130	2 S40368	Ig kappa chain - h
86	415	73.1	107	2 S36262	Ig lambda chain V
87	415	73.1	128	2 S46372	Ig light chain var
88	414	72.9	107	2 S36269	Ig lambda chain V
89	414	72.9	109	2 S31979	Ig kappa chain - h
90	413	72.7	108	1 K1HUSW	Ig kappa chain V-I
91	413	72.7	124	2 S40318	Ig kappa chain V r
92	412	72.5	95	2 PH0862	Ig kappa chain V r
93	412	72.5	108	1 K1HUGL	Ig kappa chain V-I
94	411	72.4	95	2 PH0864	Ig kappa chain V r
95	411	72.4	108	1 K1HUDE	Ig kappa chain V-I
96	411	72.4	125	2 S40316	Ig kappa chain - h
97	410	72.2	109	2 S31980	Ig kappa chain - h
98	410	72.2	109	2 S31978	Ig kappa chain - h
99	410	72.2	124	2 S40348	Ig kappa chain V-J
100	410	72.2	132	2 S38646	Ig kappa chain V r

## ALIGNMENTS

## RESULT 1

KIHUAV  
Ig kappa chain V-I region (Au) - human  
C:Species: Homo sapiens (man)  
C>Date: 24-Apr-1984 #sequence\_revision 02-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: A91653; A01862; S02573  
R:Schiechl, H.; Hillebrand, N.  
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972  
A:Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-kette vom kappa-Typ, Sub  
A:Reference number: A91653; MUID:72189444; PMID:5028201  
A:Accession: A91653  
A:Molecule type: protein  
A:Residues: 1-108 <SCH>  
A:Cross-references: UNIPROT:P01594  
A:Note: the C region of this chain has the Inv (3) marker  
R:Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Stei  
Biophys. Struct. Mech. 1, 139-146, 1975  
A:Title: The structure determination of the variable portion of the Bence-Jones protein  
A:Reference number: A90729; MUID:77022433; PMID:1234024  
A:Contents: annotation; X-ray crystallography  
A:Note: the structure of the V region was determined by molecular replacement methods us  
R:Steiner, V.; Chang, J.Y.  
FEBS Lett. 222, 6-10, 1987  
A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the  
A:Reference number: S02572; MUID:88005152; PMID:3115831  
A:Contents: annotation  
C:Comment: This is a Bence Jones protein.  
C:Genetics:

A:Gene: GDB:IGKV1  
A:Cross-references: GDB:136264  
A:Map position: 2p12-2p12  
A:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>  
F:23-88/Disulfide bonds: #status predicted

Query Match 84.5%; Score 480; DB 1; Length 108;  
Best Local Similarity 85.2%; Pred. No. 1.7e-36;  
Matches 92; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60  
DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60  
QY 61 RFSGGSGTDYTLTISSLOPEDIAFYCHQYSKLPWTFGGTKVEIKR 108  
DB 61 RFSGGSGGAHFTTISLQPEDIAFYCHQYSKLPWTFGGTKVEIKR 108

## RESULT 2

A38740  
Ig kappa chain V region (Py20) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 09-Jul-2004  
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
J. Biol. Chem. 266, 6607-6613, 1991  
A:Title: Heavy and light chain variable region sequences and antibody properties of anti  
A:Reference number: A38740; MUID:91177923; PMID:1706720  
A:Accession: A38740  
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: mRNA  
A:Residues: 1-111 <RUF>  
A:Cross-references: UNIPROT:Q91WS9  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 479; DB 2; Length 111;  
Best Local Similarity 80.6%; Pred. No. 2.2e-36;  
Matches 87; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60  
DB 4 DVQMTQTTSLSASLGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 63  
QY 61 RFSGGSGTDYTLTISSLOPEDIAFYCHQYSKLPWTFGGTKVEIKR 108  
DB 64 RFSGGSGTDYTLTISSLOPEDIAFYCHQYSKLPWTFGGTKVEIKR 111

## RESULT 3

E38740  
Ig kappa chain V region (Py54) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 09-Jul-2004  
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
J. Biol. Chem. 266, 6607-6613, 1991  
A:Title: Heavy and light chain variable region sequences and antibody properties of anti  
A:Reference number: A38740; MUID:91177923; PMID:1706720  
A:Accession: E38740  
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: mRNA  
A:Residues: 1-111 <RUF>  
A:Cross-references: UNIPROT:Q91WS9  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 477; DB 2; Length 111;  
Best Local Similarity 81.5%; Pred. No. 3.3e-36;  
Matches 88; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60  
DB 4 DVQMTQTTSLSASLGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 63  
QY 61 RFSGGSGTDYTLTISSLOPEDIAFYCHQYSKLPWTFGGTKVEIKR 108  
DB 64 RFSGGSGTDYTLTISSLOPEDIAFYCHQYSKLPWTFGGTKVEIKR 111

## RESULT 4

G38740  
Ig kappa chain V region (Py69) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 09-Jul-2004  
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
J. Biol. Chem. 266, 6607-6613, 1991  
A:Title: Heavy and light chain variable region sequences and antibody properties of anti  
A:Reference number: A38740; MUID:91177923; PMID:1706720  
A:Accession: G38740  
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: mRNA  
A:Residues: 1-111 <RUF>  
A:Cross-references: UNIPROT:Q91WS9  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 83.1%; Score 472; DB 2; Length 111;  
Best Local Similarity 81.5%; Pred. No. 9.4e-36;  
Matches 88; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60  
DB 4 DVQMTQTTSLSASLGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 63  
QY 61 RFSGGSGTDYTLTISSLOPEDIAFYCHQYSKLPWTFGGTKVEIKR 108





```
RESULT 9
S69900
Ig kappa chain (clone KL2.18 / KL4B10 / KL4C11) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69900; S69907; S69908
R:Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A:Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin 1
A:Reference number: S69900; MUID:92165291; PMID:1537587
A:Accession: S69900
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WYS>
A:Cross-references: EMBL:X55041; NID:G511023; PIDN:CAA38881.1; PID:G511024
A:Accession: S69907
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WY2>
A:Cross-references: EMBL:X55048; NID:G511037; PIDN:CAA38888.1; PID:G511038
A:Accession: S69908
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WY3>
A:Cross-references: EMBL:X55049; NID:G511039; PIDN:CAA38889.1; PID:G511040
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      81.2%; Score 461; DB 2; Length 108;
Best Local Similarity 80.6%; Pred. No. 9e-35; Indels 0; Gaps 0;
Matches 87; Conservative 10; Mismatches 11;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAVKLLIFYSNLHSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIQMTQSSLSASVGRVTITCSASQDISNYLNWYQKPKDGTGKLLIYTSRLHSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RFSGGSGTDYTLTSSLPEDIATYFCHQYSKLPWTFGQGTQKVEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 RFSGGSGTDYTLTSSLPEDIATYFCHQYSKLPWTFGQGTQKVEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
KLHURE
Ig kappa chain V-I region (Rei) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C:Accession: A91663; A01873
R:Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975
A:Title: Die Primärstruktur einer kristallinen monoklonalen Immunglobulin-L-Kette vom K
vollständige Aminosäuresequenz des Proteins.
A:Reference number: A91663; MUID:76023758; PMID:809329
A:Accession: A91663
A:Molecule type: Protein
A:Residues: 1-108 <PAL>
A:Cross-references: UNIPROT:P01607
A:Note: The C region of this chain has the Inv (1,2) marker
R:Epp, O.; Lattman, E.B.; Schiffer, M.; Huber, R.; Palm, W.
Biochemistry 14, 4943-4952, 1975
A:Title: The molecular structure of a dimer composed of the variable portions of the Ben
A:Reference number: A90393; MUID:76039968; PMID:1182131
A:Contents: annotation; X-ray crystallography, 2.0 angstroms
C:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
```

```
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status experimental

Query Match      80.3%; Score 456; DB 1; Length 108;
Best Local Similarity 80.6%; Pred. No. 2.5e-34;
Matches 87; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAVKLLIFYSNLHSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 DIQMTQSSLSASVGRVTITCSASQDIILKLNWYQQTGKAPKLLIYTSRLHSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RFSGGSGTDYTLTSSLPEDIATYFCHQYSKLPWTFGQGTQKVEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 RFSGGSGTDYTLTSSLPEDIATYFCHQYSKLPWTFGQGTQKVEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
A29380
Ig kappa chain precursor V region (AC-1001) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000
C:Accession: A29380
R:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987
A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable r
C:Keywords: heterotetramer; immunoglobulin
F:30-104/Domain: immunoglobulin homology <IMM>

Query Match      79.9%; Score 454; DB 2; Length 122;
Best Local Similarity 79.6%; Pred. No. 4.3e-34;
Matches 86; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAVKLLIFYSNLHSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 15 DIQMTQTSSLSASVGRVTITCSASQDISNYLNWYQKPKDGTGKLLIYTSRLHSGVPS 74
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RFSGGSGTDYTLTSSLPEDIATYFCHQYSKLPWTFGQGTQKVEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 75 RFSGGSGTDYTLTSSLPEDIATYFCHQYSKLPWTFGQGTQKVEIKR 122
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
S69903
Ig kappa chain (clone KL2.29 / KL2.33 / KL3.8) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69903; S69904; S69905
R:Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A:Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A:Reference number: S69900; MUID:92165291; PMID:1537587
A:Accession: S69903
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WYS>
A:Cross-references: EMBL:X55044; NID:G511029; PIDN:CAA38884.1; PID:G511030
A:Accession: S69904
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WY2>
A:Cross-references: EMBL:X55045; NID:G511031; PIDN:CAA38885.1; PID:G511032
A:Accession: S69905
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WY3>
A:Cross-references: EMBL:X55046; NID:G511033; PIDN:CAA38886.1; PID:G511034
```

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 452; DB 2; Length 108;  
Best Local Similarity 79.6%; Pred. No. 5.8e-34;  
Matches 86; Conservative 11; Mismatches 11; Indels 0; Gaps 0;  
  
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSNNLHSGVPS 60  
DB 1 DIQMTQTSLSASLGRVTISCRASQDISNYLNWYQKPKDKAVKLLIFYSNNLHSGVPS 60  
  
QY 61 RPSGGSGTDYTLTISSLOPEDIATYFCHQYSKLPWTFFGGTKVEIKR 108  
DB 61 RPSGGSGTDYTLTISSLOPEDIATYFCHQYSKLPWTFFGGTKVEIKR 108

## RESULT 13

JL0080  
Ig kappa chain precursor V region (anti-phenyloxazolone, 18C10) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 21-Jan-2000  
C;Accession: J0080  
R;Kaartinen, M.; Rocca-Serra, J.; Maelkela, O.  
Mol. Immunol. 25, 859-865, 1988  
A;Title: Combinatorial association of V genes: one VH gene codes for three non-cross-reacting B cell clones  
A;Reference number: J0080; MUID:89096973; PMID:3211160  
A;Accession: J0080  
A;Molecule type: mRNA  
A;Residues: 1-115 <XAA>  
A;Cross-references: GB:M27793; NID:g197161; PID:AAA38937.1; PID:g197162  
A;Note: the authors translated the codon AGG for residue 30 as Ser  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;1-6/Domain: signal sequence (fragment) #status predicted <SIG>  
F;7-115/Product: Ig light chain #status predicted <MAT>  
F;22-96/Domain: immunoglobulin homology <IMM>  
F;30-40/Region: complementarity-determining 1  
F;56-62/Region: complementarity-determining 2

Query Match 79.6%; Score 452; DB 2; Length 115;  
Best Local Similarity 79.6%; Pred. No. 6.2e-34;  
Matches 86; Conservative 11; Mismatches 11; Indels 0; Gaps 0;  
  
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSNNLHSGVPS 60  
DB 7 DIQMTQTSLSASLGRVTISCRASQDISNYLNWYQKPKDKAVKLLIFYSNNLHSGVPS 66  
  
QY 61 RPSGGSGTDYTLTISSLOPEDIATYFCHQYSKLPWTFFGGTKVEIKR 108  
DB 67 RPSGGSGTDYTLTISSLOPEDIATYFCHQYSKLPWTFFGGTKVEIKR 114

## RESULT 14

S52789  
Ig kappa chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C;Accession: S52789  
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the EMBL Data Library, March 1995  
A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-  
A;Reference number: S52789  
A;Accession: S52789  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-129 <ROC>  
A;Cross-references: EMBL:X85995; NID:g758589; PID:CAA59987.1; PID:g758589  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 451; DB 2; Length 129;  
Best Local Similarity 81.3%; Pred. No. 8.6e-34;

Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;  
  
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSNNLHSGVPS 60  
DB 23 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAPKLLIHASLSLETGVP 82  
  
QY 61 RPSGGSGTDYTLTISSLOPEDIATYFCHQYSKLPWTFFGGTKVEIKR 107  
DB 83 RPSGGSGTDFSTISSLOPEDLATYCCQYDNLPLTFFGGTKVEIKR 129

## RESULT 15

S44118  
Ig kappa chain V-J region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C;Accession: S44118  
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K. submitted to the EMBL Data Library, March 1994  
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable re-  
A;Reference number: S44105  
A;Accession: S44118  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-110 <HAW>  
A;Cross-references: EMBL:Z31395; NID:g472972; PID:CAA83270.1; PID:g940529  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 450; DB 2; Length 110;  
Best Local Similarity 80.9%; Pred. No. 8.9e-34;  
Matches 89; Conservative 6; Mismatches 13; Indels 2; Gaps 1;  
  
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSNNLHSGVPS 60  
DB 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAPKLLIYDASNLETGVP 60  
  
QY 61 RPSGGSGTDYTLTISSLOPEDIATYFCHQYSKLP--WTFGGTKVEIKR 108  
DB 61 RPSGGSGTDFSTISSLOPEDIATYCCQYDNLPPGVTFPGTKVDIKR 110

Search completed: August 1, 2005, 09:18:44  
Job time : 7.11574 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:55 ; Search time 28.0249 Seconds  
(without alignments)  
1973.408 Million cell updates/sec

Title: US-10-089-500-54

Perfect score: 568

Sequence: 1 DIQMTQSPSLSSASVGRVT.....HOYSKLPWTFGGQTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	480	84.5	108	1	KV1B HUMAN
2	461	81.2	108	1	KV5J MOUSE
3	456	80.3	108	1	KV10 HUMAN
4	448	78.9	108	1	KV5K MOUSE
5	447	78.7	108	1	KV5L MOUSE
6	447	78.7	108	1	KV5M MOUSE
7	445	78.3	108	1	KV1A HUMAN
8	445	78.3	108	2	Q9UL77
9	445	78.3	108	2	Q9UL77
10	443	78.0	108	1	KV5N MOUSE
11	439	77.3	236	2	Q6GMW1
12	438	77.1	108	1	KV1P HUMAN
13	436	76.8	108	1	KV1Y HUMAN
14	434	76.4	108	2	Q9UL70
15	433.5	76.3	107	2	Q96SA9
16	433	76.2	108	1	KV1R HUMAN
17	433	76.2	236	2	Q6GMX9
18	430	75.7	108	1	KV5U MOUSE
19	430	75.7	236	2	Q723Y4
20	429	75.5	107	2	Q9JL84
21	429	75.5	108	1	KV1M HUMAN
22	427	75.2	236	2	Q6GMX8
23	424	74.6	236	2	KV1H HUMAN
24	423	74.5	236	2	Q6GMX0
25	422	74.3	129	1	KV1W HUMAN
26	420	73.9	108	1	KV1K HUMAN
27	420	73.9	108	1	KV1Q HUMAN
28	419	73.8	108	1	KV1V HUMAN
29	418	73.6	108	1	KV1L HUMAN
30	417	73.4	108	1	KV1C HUMAN
31	416.5	73.3	107	2	Q9UL81
					P01594 homo sapien
					P01643 mus musculus
					P01607 homo sapien
					P01644 mus musculus
					P01645 mus musculus
					P01646 mus musculus
					P01593 homo sapien
					P01648 mus musculus
					Q9UL77 homo sapien
					P01647 mus musculus
					Q6GMW1 homo sapien
					P01608 homo sapien
					P80362 homo sapien
					Q9UL70 homo sapien
					Q96SA9 homo sapien
					P01610 homo sapien
					Q6GMX9 homo sapien
					P04946 mus musculus
					Q723Y4 homo sapien
					Q9JL84 mus musculus
					P01605 homo sapien
					Q6GMX8 homo sapien
					P01600 homo sapien
					Q6GMX0 homo sapien
					P04431 homo sapien
					P01603 homo sapien
					P01609 homo sapien
					P04430 homo sapien
					P01604 homo sapien
					P01595 homo sapien
					Q9UL81 homo sapien

ALIGNMENTS

32	416	73.2	108	1	KVIN HUMAN	P01606 homo sapien
33	416	73.2	116	2	Q9EPF6	Q9EPF6 homo sapien
34	414	72.9	236	2	Q6PIH7	Q6PIH7 homo sapien
35	413	72.7	108	1	KVIS HUMAN	P01611 homo sapien
36	413	72.7	244	2	Q6SZC8	Q6SZC8 homo sapien
37	412	72.5	108	1	KVIG HUMAN	P01599 homo sapien
38	411	72.4	108	1	KVIF HUMAN	P01597 homo sapien
39	411	72.4	234	2	Q7Z473	Q7Z473 homo sapien
40	408.5	71.9	107	1	KVID HUMAN	P01596 homo sapien
41	408	71.8	240	2	Q652C9	Q652C9 homo sapien
42	405.5	71.4	109	1	KVIT HUMAN	P01612 homo sapien
43	403	71.0	108	2	Q9UL79	Q9UL79 homo sapien
44	400	70.4	108	1	KVIF HUMAN	P01598 homo sapien
45	394	69.4	236	2	Q6PIH4	Q6PIH4 homo sapien
46	394	69.4	236	2	Q6PIH5	Q6PIH5 homo sapien
47	393	69.2	134	1	KV4C HUMAN	P06314 homo sapien
48	388	68.3	108	1	KV5S MOUSE	P01652 mus musculus
49	388	68.3	129	1	KV1X HUMAN	P04432 homo sapien
50	384	67.6	130	1	KV5Q MOUSE	P01639 mus musculus
51	379	66.7	108	1	KV5Q MOUSE	P01650 mus musculus
52	379	66.7	117	1	KVII HUMAN	P01601 homo sapien
53	376	66.2	236	2	Q7TS98	Q7TS98 mus musculus
54	374	65.8	108	1	KV5P MOUSE	P01649 mus musculus
55	373	65.7	108	1	KV5T MOUSE	P01653 mus musculus
56	373	65.7	109	2	Q920E6	Q920E6 mus musculus
57	373	65.7	112	1	KVIU HUMAN	P01613 homo sapien
58	371	65.3	114	1	KV4A HUMAN	P01625 homo sapien
59	371	65.3	117	1	KVIJ HUMAN	P01602 homo sapien
60	368	64.8	108	1	KV5R MOUSE	P01651 mus musculus
61	365	64.3	128	1	KV5E MOUSE	P01637 mus musculus
62	362.5	63.8	129	1	KV3M HUMAN	P18136 homo sapien
63	362.5	63.8	133	1	KV4B HUMAN	P06313 homo sapien
64	360.5	63.5	243	2	Q7TQM2	Q7TQM2 mus musculus
65	359	63.2	127	2	Q925S9	Q925S9 mus musculus
66	357.5	62.9	110	1	KV3P MOUSE	P01668 mus musculus
67	357	62.9	298	2	Q9QYF0	Q9QYF0 synthetic c
68	356	62.7	111	1	KV3O MOUSE	P01667 mus musculus
69	356	62.7	111	1	KV3Q MOUSE	P01669 mus musculus
70	355.5	62.6	109	1	KV3D HUMAN	P01622 homo sapien
71	355.5	62.6	134	2	Q8VDD0	Q8VDD0 mus musculus
72	353.5	62.2	109	1	KV3B HUMAN	P01620 homo sapien
73	353.5	62.2	109	1	KV3E HUMAN	P01623 homo sapien
74	353.5	62.2	129	1	KV3H HUMAN	P04207 homo sapien
75	353.5	62.2	129	1	KV3L HUMAN	P18135 homo sapien
76	353	62.1	238	2	Q6GJS7	Q6GJS7 mus musculus
77	352	62.0	108	2	Q8VIJ0	Q8VIJ0 mus musculus
78	351	61.8	108	1	KV5D MOUSE	P01636 mus musculus
79	350.5	61.7	109	1	KV3F HUMAN	P01624 homo sapien
80	350.5	61.7	112	2	Q8K1F3	Q8K1F3 mus musculus
81	349	61.4	136	1	KV5B MOUSE	P01634 mus musculus
82	347.5	61.2	109	2	Q9UL78	Q9UL78 homo sapien
83	347	61.1	149	1	KV5A MOUSE	P01633 mus musculus
84	346	60.9	108	2	Q9UL83	Q9UL83 homo sapien
85	346	60.9	111	1	KV3M MOUSE	P01665 mus musculus
86	345.5	60.8	114	2	Q8K1F1	Q8K1F1 mus musculus
87	345.5	60.8	235	2	Q6GMW0	Q6GMW0 homo sapien
88	345	60.7	112	1	KV3G MOUSE	P01659 mus musculus
89	343	60.4	132	1	KV3F MOUSE	P01658 mus musculus
90	342.5	60.3	112	2	Q8K1F2	Q8K1F2 mus musculus
91	342	60.2	111	1	KV3L MOUSE	P01664 mus musculus
92	342	60.2	111	2	Q920E9	Q920E9 mus musculus
93	340	59.9	111	1	KV3N MOUSE	P01666 mus musculus
94	339.5	59.8	235	2	Q6PJF2	Q6PJF2 homo sapien
95	339	59.7	111	1	KV3A MOUSE	P01654 mus musculus
96	338	59.5	109	1	KV4D HUMAN	P81593 homo sapien
97	338	59.5	262	2	Q6SZI1	Q6SZI1 mus musculus
98	337	59.3	111	1	KV3R MOUSE	P01670 mus musculus
99	337	59.3	111	1	KV3S MOUSE	P01671 mus musculus
100	337	59.3	131	1	KV3I MOUSE	P01661 mus musculus



21-JUL-1986 (Rel. 01, Last sequence update)  
 25-OCT-2004 (Rel. 45, Last annotation update)  
 Ig kappa chain V-I region Rel. 11  
 Homo sapiens (Human)  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 SEQUENCE.  
 RP MEDLINE=76023758; PubMed=809329;  
 RA Palm W., Hilschmann N.;  
 RT "The primary structure of a crystalline monoclonal immunoglobulin  
 kappa-type I-chain, subgroup I (Bence-Jones protein Rel); isolation  
 and characterization of the tryptic peptides; the complete amino acid  
 sequence of the protein; a contribution to the elucidation of the  
 three-dimensional structure of antibodies, in particular their  
 combining site.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191 (1975).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RA MEDLINE=76039968; PubMed=1182131;  
 RX Epp O., Lattman E.B., Schiffer M., Huber R., Palm W.;  
 RT "The molecular structure of a dimer composed of the variable portions  
 of the Bence-Jones protein Rel refined at 2.0-A resolution.";  
 RL Biochemistry 14:4943-4952 (1975).  
 CC -I- MISCELLANEOUS: The C region of this chain has the INV (1,2)  
 marker.  
 CC -I- MISCELLANEOUS: This is a Bence-Jones protein.  
 DR PIR; A91663; KIHURE.  
 DR PDB; 1AR2; X-ray; @=1-107.  
 DR PDB; 1BWW; X-ray; A/B=1-107.  
 DR PDB; 1REI; X-ray; A/B=1-107.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 DR 3D-structure; Bence-Jones protein; Direct protein sequencing;  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 34 Complementarity-determining-1.  
 FT DOMAIN 35 49 Framework-2.  
 FT DOMAIN 50 56 Complementarity-determining-2.  
 FT DOMAIN 57 88 Framework-3.  
 FT DOMAIN 89 97 Complementarity-determining-3.  
 FT DOMAIN 98 107 Framework-4.  
 FT DISULFID 23 88  
 FT STRAND 4 7  
 FT STRAND 10 13  
 FT STRAND 15 16  
 FT STRAND 19 25  
 FT STRAND 30 31  
 FT STRAND 33 38  
 FT STRAND 40 41  
 FT STRAND 45 49  
 FT STRAND 50 52  
 FT STRAND 53 54  
 FT STRAND 56 57  
 FT STRAND 60 61  
 FT STRAND 62 67  
 FT STRAND 68 69  
 FT STRAND 70 75  
 FT STRAND 80 82  
 FT STRAND 84 90  
 FT STRAND 97 98  
 FT STRAND 102 106  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;  
 Query Match 80.3%; Score 456; DB 1; Length 108;

Best Local Similarity 80.6%; Pred. No. 3.2e-40;  
 Matches 87; Conservative 7; Mismatches 14; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVITTCASQDINSYLNWYQOKPKAVKLLIFYSNLSHGVPS 60  
 DB 1 DIQMTQSPSSLSASVGRVITTCASQDINSYLNWYQOKPKAVKLLIFYSNLSHGVPS 60  
 QY 61 RFSGSGSGTDYTLTISSLPEDVATYFCHQYKSLPWTFGQGTKEIKR 108  
 DB 61 RFSGSGSGTDYTLTISSLPEDVATYFCHQYKSLPWTFGQGTKEIKR 108  
 RESULT 4  
 KVSK MOUSE  
 ID KVSK MOUSE STANDARD; PRT; 108 AA.  
 AC P01644;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig kappa chain V-V region HP R16.7.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=A/J;  
 RX MEDLINE=82150934; PubMed=6801658;  
 RA Siegelman M., Capra J.D.;  
 RT "Complete amino acid sequence of light chain variable regions derived  
 from five monoclonal anti-p-azophenylarsenate antibodies differing  
 with respect to a crossreactive idiotype.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683 (1981).  
 CC -I- MISCELLANEOUS: Anti-arsenate hybridoma protein.  
 DR PIR; A01927; KMSAR.  
 DR HSSP; P01594; IJVS.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin V region.  
 FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 34 Complementarity-determining-1.  
 FT DOMAIN 35 49 Framework-2.  
 FT DOMAIN 50 56 Complementarity-determining-2.  
 FT DOMAIN 57 88 Framework-3.  
 FT DOMAIN 89 97 Complementarity-determining-3.  
 FT DOMAIN 98 108 Framework-4.  
 FT DISULFID 23 88 By similarity.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFP597 CRC64;  
 Query Match 78.9%; Score 448; DB 1; Length 108;  
 Best Local Similarity 79.6%; Pred. No. 2.2e-39;  
 Matches 86; Conservative 10; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVITTCASQDINSYLNWYQOKPKAVKLLIFYSNLSHGVPS 60  
 DB 1 DIQMTQSPSSLSASVGRVITTCASQDINSYLNWYQOKPKAVKLLIFYSNLSHGVPS 60  
 QY 61 RFSGSGSGTDYTLTISSLPEDVATYFCHQYKSLPWTFGQGTKEIKR 108  
 DB 61 RFSGSGSGTDYTLTISSLPEDVATYFCHQYKSLPWTFGQGTKEIKR 108  
 RESULT 5  
 KVSL MOUSE  
 ID KVSL MOUSE STANDARD; PRT; 108 AA.  
 AC P01645;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 05-JUL-2004 (Rel. 44, Last annotation update)

```
DE Ig kappa chain V-V region HP 93G7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSP; P01607; IRII.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; Igv; 1.
DR PFAM; PF00047; ig; 1.
DR QMART; QM00406; Igv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Complementarity-determining-2.
FT DOMAIN 50 56 Complementarity-determining-3.
FT DOMAIN 57 88 Complementarity-determining-4.
FT DOMAIN 89 97 By similarity.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFPF58E CRC64;

Query Match 78.7%; Score 447; DB 1; Length 108;
Best Local Similarity 79.6%; Pred. No. 2.9e-39;
Matches 86; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAVKLLIFYSNLSHGVPVS 60
DB 1 DIQMTQSTSSLSASLGDRVTISCRASQDISNYLNWYQKPKDGTGTVKLLIYTSRLSHGVPVS 60

QY 61 RFSGGSGTDYLTITSSLPEDIATYFCHQYSKLPWTFGQGTKEIKR 108
DB 61 RFSGGSGTDYLTITSSLPEDIATYFCHQYSKLPWTFGQGTKEIKR 108

RESULT 6
KV5M_MOUSE
ID KV5M_MOUSE STANDARD; PRT; 108 AA.
AC P01646;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 123E6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSP; P01594; IJVS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR PFAM; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.

Query Match 78.7%; Score 447; DB 1; Length 108;
Best Local Similarity 79.6%; Pred. No. 2.9e-39;
Matches 86; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAVKLLIFYSNLSHGVPVS 60
DB 1 DIQMTQSTSSLSASLGDRVTISCRASQDISNYLNWYQKPKDGTGTVKLLIYTSRLSHGVPVS 60

QY 61 RFSGGSGTDYLTITSSLPEDIATYFCHQYSKLPWTFGQGTKEIKR 108
DB 61 RFSGGSGTDYLTITSSLPEDIATYFCHQYSKLPWTFGQGTKEIKR 108

RESULT 7
KV1A_HUMAN
ID KV1A_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01861; KIHUAG.
DR HSP; P01607; 1BMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR PFAM; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Complementarity-determining-2.
FT DOMAIN 50 56 Complementarity-determining-3.
FT DOMAIN 57 88 Complementarity-determining-4.
FT DOMAIN 89 97 By similarity.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 78.3%; Score 445; DB 1; Length 108;
Best Local Similarity 78.7%; Pred. No. 4.7e-39;
Matches 85; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
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FT NON TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EFFA2 CRC64;

Query Match 77.3%; Score 439; DB 2; Length 236;
Best Local Similarity 81.3%; Pred. No. 5.1e-38;
Matches 87; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 2 IQMTQSPSSLSASVGDRTVITCSASQDISNLYNWKQPKAVKLLIFYSNLSHGVPFR 61
DB 24 IQMTQSPSSLSASVGDRTVITCSASQDISNLYNWKQPKAVKLLIFYSNLSHGVPFR 83

QY 62 FSGGSGTDYTLTSSLOPEDIAFYCHQYKLPWTFQGTKEIKR 108
DB 84 FSGGSGTDYTLTSSLOPEDIAFYCHQYKLPWTFQGTKEIKR 130

RESULT 12
KVLP_HUMAN STANDARD; PRT; 108 AA.
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-I region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hillechmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
Cum.)";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hillechmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
Steinmetz-Kayne M., Suter L., Watanabe S.;
RA (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New
York (1969).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91638; KIHURY.
DR HSPR; P01607; 1BWV.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match 77.1%; Score 438; DB 1; Length 108;
Best Local Similarity 78.7%; Pred. No. 2.5e-38;
Matches 85; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWKQPKAVKLLIFYSNLSHGVPFR 60
DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWKQPKAVKLLIFYSNLSHGVPFR 60

QY 61 FSGGSGTDYTLTSSLOPEDIAFYCHQYKLPWTFQGTKEIKR 108
DB 61 FSGGSGTDYTLTSSLOPEDIAFYCHQYKLPWTFQGTKEIKR 108

RESULT 11
Q6GMW1 PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.B., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BF6EA087AFAC437 CRC64;
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Qy 61 RFGSGSGTDYTLTISSLPEDIATYFCHQYSLPWTFGQTKVEIKR 108  
 Db 61 RFGSGSGTDFTFTISSLPEDIATYFCHQYSLPWTFGQTKVEIKR 108

RESULT 13  
 KVIY\_HUMAN STANDARD; PRT; 108 AA.  
 ID KVIY\_HUMAN  
 AC P80362;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Ig kappa chain V-1 region WAT.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=95086080; PubMed=7993911;  
 RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,  
 RA Solomon A., Stevens F.J., Schiffer M.;  
 RT "Comparison of crystal structures of two homologous proteins:  
 RT structural origin of altered domain interactions in immunoglobulin  
 RT light-chain dimers.";  
 RL Biochemistry 33:14848-14857(1994).  
 RN [2]  
 SEQUENCE OF 1-35.  
 RX MEDLINE=81267384; PubMed=6167731;  
 RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,  
 RA Popp R.A., Solomon A.;  
 RT "Characterization and preliminary crystallographic data on the VL-  
 RT related fragment of the human kappa Bence Jones protein Wat.";  
 RL J. Mol. Biol. 147:185-193(1991).  
 CC 1- MISCELLANEOUS: This is a Bence-Jones protein.  
 DR PDB; 1WU; X-ray; A/B=1-108.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 DR 3D-structure; Bence-Jones protein; Direct protein sequencing;  
 KW Immunoglobulin V region.  
 PT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 34 Complementarity-determining-1.  
 FT DOMAIN 35 49 Framework-2.  
 FT DOMAIN 50 56 Complementarity-determining-2.  
 FT DOMAIN 57 88 Framework-3.  
 FT DOMAIN 89 97 Complementarity-determining-3.  
 FT DOMAIN 98 107 Framework-4.  
 FT DISULFID 23 88 By similarity.  
 FT CONFLICT 30 31 TN -> SD (in Ref. 2).  
 FT STRAND 4 7  
 FT STRAND 10 13  
 FT TURN 15 16  
 FT TURN 19 25  
 FT TURN 30 31  
 FT STRAND 33 38  
 FT TURN 40 41  
 FT STRAND 45 49  
 FT TURN 50 52  
 FT TURN 53 54  
 FT TURN 56 57  
 FT STRAND 60 61  
 FT TURN 62 67  
 FT STRAND 68 69  
 FT STRAND 70 75  
 FT HELIX 80 82  
 FT STRAND 84 90  
 FT STRAND 98 98

FT STRAND 102 106  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAB697 CRC64;

Query Match 76.8%; Score 436; DB 1; Length 108;  
 Best Local Similarity 76.9%; Pred. No. 4.1e-38;  
 Matches 83; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCASQDISNYLNWYQOKPKDKAVKLLIFVSSNLHSGVPS 60  
 Db 1 DIQMTQSPSSLSASVGRVITTCASQDISNYLNWYQOKPKDKAVKLLIFVSSNLHSGVPS 60

Qy 61 RFGSGSGTDYTLTISSLPEDIATYFCHQYSLPWTFGQTKVEIKR 108  
 Db 61 RFGSGSGTDFTFTISSLPEDIATYFCHQYSLPWTFGQTKVEIKR 108

RESULT 14  
 Q9UL70 PRELIMINARY; PRT; 108 AA.  
 ID Q9UL70;  
 AC Q9UL70;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
 RA Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035044; AAD56280.1; --  
 DR PIR; PH0863; PH0863.  
 DR HSSP; P01607; LBWW.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 76.4%; Score 434; DB 2; Length 108;  
 Best Local Similarity 77.8%; Pred. No. 6.7e-38;  
 Matches 84; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCASQDISNYLNWYQOKPKDKAVKLLIFVSSNLHSGVPS 60  
 Db 1 DIQMTQSPSSLSASVGRVITTCASQDISNYLNWYQOKPKDKAVKLLIFVSSNLHSGVPS 60

Qy 61 RFGSGSGTDYTLTISSLPEDIATYFCHQYSLPWTFGQTKVEIKR 108  
 Db 61 RFGSGSGTDFTFTISSLPEDIATYFCHQYSLPWTFGQTKVEIKR 108

RESULT 15  
 Q96SA9 PRELIMINARY; PRT; 107 AA.  
 ID Q96SA9  
 AC Q96SA9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain  
 DE variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic arthritis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSP; P01607; 1BWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 76.3%; Score 433.5; DB 2; Length 107;
Best Local Similarity 81.7%; Pred. No. 7.5e-38;
Matches 89; Conservative 6; Mismatches 11; Indels 3; Gaps 2;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDLSNVLNMYQOKPKAVKLLIFYSNLSHGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSISSVLNMYQOKPKAPKLLIYAASSLSQGVPS 60

Qy 61 RFSGSGSGTDYTLTISSLPEDFATYYCQSYSTL--TFGGGTKVEIKR 108
Db 61 RFSGSGSGTDFTLTISLPEDFATYYCQSYSTL--TFGGGTKVEIKR 107

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Search completed: August 1, 2005, 09:17:09  
 Job time : 28.0249 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:10 ; Search time 35.8407 Seconds  
(without alignments)  
1284.140 Million cell updates/sec

Title: US-10-089-500-55  
Perfect score: 624  
Sequence: 1 EVTLVSGGDFVRPGSLKV.....KLCTYFDSWGQGTTLTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq\_16Dec04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003s.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624	100.0	119	4	AAB81989
2	624	100.0	119	6	ABU11012
3	624	100.0	130	2	AAR33256
4	624	100.0	130	2	AAR53341
5	624	100.0	130	2	AAY28369
6	624	100.0	130	3	AAB01627
7	624	100.0	138	4	AAB81977
8	624	100.0	138	6	ABU11002
9	624	100.0	582	4	AAB81991
10	579	92.8	119	4	AAB81985
11	579	92.8	119	6	ABU11010
12	579	92.8	582	4	AAB81987
13	493	79.0	119	2	AAB29994
14	487	78.0	134	6	ABP60555
15	486.5	78.0	294	4	AAB20442
16	486.5	78.0	325	4	AAB20438
17	486.5	78.0	732	4	AAB20437
18	486	77.9	140	6	ABG74241
19	486	77.9	247	2	AAW11917
20	482.5	77.3	249	4	AAB20436
21	481	77.1	121	5	AAE16426
22	480.5	77.0	121	6	ABR41818
23	480	76.9	119	2	AAB29996
24	480	76.9	237	7	AAE38657
25	477.5	76.5	121	8	ADM78071

26	477	76.4	232	7	ADF72730
27	477	76.4	241	7	ADF72729
28	477	76.4	255	7	ADF72734
29	475.5	76.2	249	4	AAB20435
30	475	76.1	119	5	AAU72814
31	475	76.1	119	6	AAO29882
32	475	76.1	119	7	ADJ79825
33	475	76.1	249	4	AAB20434
34	475	76.1	462	6	AAO29869
35	475	76.1	462	7	ADJ79787
36	475	76.1	464	5	AAU72801
37	473.5	75.9	120	5	AAO18391
38	473.5	75.9	468	8	ADQ07413
39	473.5	75.9	468	8	ADQ12196
40	473	75.8	123	8	ADR38656
41	472	75.6	119	2	AAR79887
42	472	75.6	239	2	AAR79866
43	471	75.5	262	6	ABR42295
44	471	75.5	262	6	ABR42293
45	471	75.5	262	6	ABR42290
46	471	75.5	262	6	ABR42291
47	471	75.5	268	6	ABR42288
48	471	75.5	268	6	ABR42287
49	471	75.5	268	6	ABR42286
50	471	75.5	268	6	ABR83643
51	471	75.5	415	6	AAR79888
52	470	75.3	119	2	AAR79876
53	469	75.2	119	2	AAR79876
54	469	75.2	247	7	ADC03132
55	469	75.2	262	6	ABR42298
56	469	75.2	268	6	ABR42297
57	469	75.2	268	6	ABR83644
58	468.5	75.1	118	2	AAW57576
59	468.5	75.1	118	2	AAW89627
60	468.5	75.1	118	3	AAV77502
61	468.5	75.1	118	4	AAW76918
62	468.5	75.1	118	4	AAW76880
63	468.5	75.1	118	4	AAW64764
64	468.5	75.1	118	4	AAW63382
65	468.5	75.1	118	4	AAW76899
66	468.5	75.1	118	5	ABW95197
67	468.5	75.1	118	6	ABJ36649
68	468.5	75.1	118	8	ADO33843
69	468.5	75.1	137	2	AAW57592
70	468.5	75.1	137	2	AAW89625
71	468.5	75.1	137	3	AAW77513
72	468.5	75.1	137	4	AAW67102
73	468.5	75.1	137	4	AAW64775
74	468.5	75.1	137	4	AAW64775
75	468.5	75.1	137	5	ABW95208
76	468.5	75.1	137	6	ABJ36667
77	468.5	75.1	137	8	ADO33883
78	468	75.0	140	5	AAU76122
79	468	75.0	144	5	ABW79730
80	468	75.0	155	6	ABP72295
81	468	75.0	155	8	ADQ15508
82	468	75.0	165	6	ABP72294
83	468	75.0	165	8	ADQ15506
84	467	74.8	158	8	ADL27491
85	466.5	74.8	118	2	AAW41233
86	466	74.7	115	8	ADW85733
87	466	74.7	115	8	ADL23071
88	465.5	74.6	120	5	AAO18395
89	465	74.5	117	6	ABW55318
90	465	74.5	119	8	ADR47407
91	465	74.5	119	8	ADR47405
92	465	74.5	138	8	ADR47397
93	465	74.5	144	8	ADR47417
94	465	74.5	247	1	AAW80156
95	464	74.4	119	3	AAW79424
96	464	74.4	138	2	AAW20064
97	463	74.2	140	5	AAW76132
98	462	74.0	123	6	AAO27198

Adf72730	Divalent
Adf72729	Monovalen
Adf72734	His-tagge
Aab20435	Anti-FIX/
Aau72814	Humanised
Aao29882	M type fu
Adj79825	M-type hu
Adj20434	Anti-FIX/
Aao29869	Mouse ant
Adj79787	TRA-8 ant
Aau72801	TRA-8 hea
Aao18391	Murine CB
Adq07413	Mature CB
Adq12196	CBE11 pen
Adr38656	Mouse hea
Aar79887	Anti-EGFR
Aar79866	Anti-EGFR
Aar42295	Bispecifi
Aar42293	Bispecifi
Aar42290	Diabody h
Aar42291	Bispecifi
Abr42288	Diabody 6
Abr42287	Diabody 6
Abr42286	Diabody 6
Abr83643	679-scFv
Abr83644	h679-scFv
Aaw57576	Chimeric
Aaw89627	Mouse hum
Aay77502	Peptide s
Aab76918	Human PTH
Aab76880	Human PTH
Aag64764	Mouse ant
Aag63382	Amino aci
Aab76899	Human PTH
Abb95197	Mouse joi
Abj36649	Angiogene
Ado33843	Murine pa
Aaw57592	Chimeric
Aaw89625	Mouse hum
Aay77513	Mouse ant
Aag67102	Amino aci
Aag64775	Mouse ant
Aag63393	Amino aci
Abb95208	Mouse joi
Abj36667	Angiogene
Ado33883	Murine pa
Aau76122	Mouse mon
Abb79730	Anti-Stre
Abp72295	Chimeric
Adq15508	Dhvar1-11
Abp72294	Chimeric
Adq15506	Histatin
Adl27491	Amino aci
Aar41233	Monoclonal
Ade85733	Human Eph
Adl23071	Human Eph
Aao18395	Humanised
Abr55318	Variable
Adr47407	Heavy cha
Adr47405	IC8 VH do
Adr47397	Heavy cha
Adr47417	Heavy cha
Aap80156	Bioynthe
Aar79424	Tie2 rece
Aar20064	MRK16-H c
Aaw76132	Mouse mAb
Aao27198	Murine an

99 462 74.0 123 7 ADC84583 Adc84583 CDR3 high  
100 462 74.0 123 8 ADH50839 Adh50839 Mouse ant

ALIGNMENTS

RESULT 1

AAB81989

ID AAB81989 standard; protein; 119 AA.

AC AAB81989;

DT 03-JUL-2001 (first entry)

XX

DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 55.

XX

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.

XX

OS Mus musculus.

PN WO200123432-A1.

XX

PD 05-APR-2001.

XX

PF 29-SEP-2000; 2000WO-JP006774.

XX

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

XX

PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX

PI Hanai N, Shitara K, Nakamura K, Niwa R;

XX

DR WPI; 2001-266143/27.

XX

PT New human type complementation-determining region-transplanted antibody,  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.

XX

PS Claim 10; Page 173-174; 183pp; Japanese.

XX

CC The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumours, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention

XX

SQ Sequence 119 AA;

Query Match 100.0%; Score 624; DB 4; Length 119;

Best Local Similarity 100.0%; Pred. No. 7.8e-51;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAFASHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60

DB 1 EVTLVESGGDFVKPGGSLKVSAAAGFAFASHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFYFDSWGQGTTLTVSS 119

DB 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFYFDSWGQGTTLTVSS 119

RESULT 2

ABU11012

ID ABU11012 standard; protein; 119 AA.

AC ABU11012;

XX

DT 04-FEB-2003 (first entry)

XX

DE Modified ganglioside GD3 antibody associated protein #5.  
XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.  
KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

OS Mus musculus.

PN WO200278739-A1.

XX

PD 10-OCT-2002.

XX

PF 29-MAR-2002; 2002WO-JP003170.

XX

PR 29-MAR-2001; 2001JP-00097483.

XX

PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX

PI Shitara K, Niwa R, Kanazawa J, Asada M;

XX

DR WPI; 2003-067410/06.

XX

PT Drugs containing genetically-modified antibody against ganglioside GD3,  
PT its fragment, immunocompetent cell activators or/and antitumor agents in  
PT combination, applicable in treating malignant tumor like melanoma.

XX

PS Claim 7; Page 112-113; 121pp; Japanese.

XX

CC The invention describes drugs contain a genetically-modified antibody  
CC against ganglioside GD3 or its fragment and at least 1 of a substance  
CC capable of activating immunocompetent cells and a substance having an  
CC antitumor activity in combination. The drugs can be used to treat tumour  
CC like melanoma and can provide a treatment with enhanced therapeutic  
CC effect and little side-reactions, particularly to relieve problems of  
CC side-effects during the conventional single administration. This sequence  
CC represents a protein associated with the anti- ganglioside GD3 antibody

XX

SQ Sequence 119 AA;

Query Match 100.0%; Score 624; DB 6; Length 119;

Best Local Similarity 100.0%; Pred. No. 7.8e-51;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAFASHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60

DB 1 EVTLVESGGDFVKPGGSLKVSAAAGFAFASHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFYFDSWGQGTTLTVSS 119

DB 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFYFDSWGQGTTLTVSS 119

RESULT 3

AAR33256

ID AAR33256 standard; protein; 130 AA.

XX

AC AAR33256;

XX

DT 25-MAR-2003 (revised)

DT 12-JUL-1993 (first entry)

XX

DE Rat immunoglobulin H chain variable region of pKM641HA3.

XX

KW Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;

KW humanised; chimeric; antibody; expression vector.

XX

OS Rattus rattus.

XX

FT Key Location/Qualifiers

FT Peptide 1..10

FT Protein /note= "Signal peptide"

FT Protein 11..130

FT Protein /note= "Mature protein"

XX

PN EP533199-A2.

XX PD 24-MAR-1993.  
 XX XX  
 XX PF 18-SEP-1992; 92EP-00116026.  
 XX XX  
 XX PR 18-SEP-1991; 91JP-00238375.  
 XX XX  
 XX PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.  
 XX XX  
 XX PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;  
 XX XX  
 XX DR WPI; 1993-095510/12.  
 XX DR N-PSDB; AAQ33257.  
 XX XX  
 XX PT Humanised chimeric antibody prodn. against ganglioside GD3 - for treating  
 XX PT cancers, such as melanoma, neuroblastoma, etc.  
 XX PT  
 XX PS Claim 6; Page 29-30; 63pp; English.  
 XX XX  
 CC The sequences given in AAR33256-57 represent rat heavy and light chain  
 CC variable regions respectively. The DNA sequences encoding these proteins  
 CC were used in the construction of humanised chimeric antibody expression  
 CC vectors. In these humanised antibodies none of the amino acids of the non  
 CC -human animal Ab variable region have been changed. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 XX XX  
 XX SQ Sequence 130 AA;  
 Query Match 100.0%; Score 624; DB 2; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-51;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EVTLVSGGDFVKPGSLKVSACAAGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSTYY 60  
 DB 11 EVTLVSGGDFVKPGSLKVSACAAGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSTYY 70  
 QY 61 SDSVKGRTISRDNKNTLYLQWRSLSRSDSAMFYCTRVKLGTYTFDSWGQGTTLTVSS 119  
 DB 71 SDSVKGRTISRDNKNTLYLQWRSLSRSDSAMFYCTRVKLGTYTFDSWGQGTTLTVSS 129  
 RESULT 4  
 AAR53341  
 ID AAR53341 standard; protein; 130 AA.  
 XX AC AAR53341;  
 XX DT 18-NOV-1994 (first entry)  
 XX DE KM641 L chain variable region.  
 XX KW Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;  
 KW expression vector; heavy; light; chain; hypervariable region; CDR;  
 KW constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.  
 XX OS Mus musculus.  
 XX FH Key Location/Qualifiers  
 FT Peptide 1..10  
 FT /label= eig\_peptide  
 XX XX  
 XX PN AU9346181-A.  
 XX PD 17-MAR-1994.  
 XX PF 07-SEP-1993; 93AU-00046181.  
 XX PR 07-SEP-1992; 92JP-00238452.  
 XX XX  
 XX PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX XX  
 XX PI Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;  
 XX XX

DR WPI; 1994-126857/16.  
 DR N-PSDB; AAQ45439.  
 XX Humanised antibody specific for ganglioside GM2 - used for producing a  
 PT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.  
 XX XX  
 XX PS Example 2; Page 116-117; 191pp; English.  
 XX XX  
 CC Example 2 describes the construction of the vector pCh1641HA1 for  
 CC chimeric human antibody H chain expression. mRNA from mouse anti-CD3  
 CC monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain  
 CC cDNAs isolated. The base sequences of the Ig variable regions in KM641 H  
 CC chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in  
 CC AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector  
 CC was constructed by joining the H chain variable region gene from  
 CC pKM641HA3 to a vector for chimeric human Ab H chain expression using the  
 CC synthetic DNAs given in AAQ63439 and AAQ63440  
 XX XX  
 XX SQ Sequence 130 AA;  
 Query Match 100.0%; Score 624; DB 2; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-51;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EVTLVSGGDFVKPGSLKVSACAAGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSTYY 60  
 DB 11 EVTLVSGGDFVKPGSLKVSACAAGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSTYY 70  
 QY 61 SDSVKGRTISRDNKNTLYLQWRSLSRSDSAMFYCTRVKLGTYTFDSWGQGTTLTVSS 119  
 DB 71 SDSVKGRTISRDNKNTLYLQWRSLSRSDSAMFYCTRVKLGTYTFDSWGQGTTLTVSS 129  
 RESULT 5  
 AAY28369  
 ID AAY28369 standard; protein; 130 AA.  
 XX AC AAY28369;  
 XX DT 04-NOV-1999 (first entry)  
 XX DE pKM641 HA3 immunoglobulin heavy chain.  
 XX KW antibody; nucleotide; genomic; hypervariable region; chimeric;  
 KW light chain; amino acid.  
 XX OS Mus sp.  
 XX PN US5939532-A.  
 XX PD 17-AUG-1999.  
 XX PF 07-JUN-1995; 95US-00483528.  
 XX PR 07-SEP-1993; 93US-00116778.  
 XX XX  
 XX PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX XX  
 XX PI Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;  
 XX DR WPI; 1999-468416/39.  
 XX DR N-PSDB; AAX99482.  
 XX XX  
 XX PT Chimeric human antibody expression vectors.  
 XX PS Example 1; Col 99-101; 188pp; English.  
 XX XX  
 CC This immunoglobulin region was isolated from pKM641HA3. This sequence has  
 CC no methionine initiation codon and the leader sequence was partly  
 CC lacking. The chimeric human antibodies are useful in the treatment of  
 CC cancer, especially that which is of neural ectodermal origin. In contrast  
 CC to prior art constructs based on mouse monoclonal antibodies, the  
 CC chimeric human antibodies do not cause anti-mouse immunoglobulin

CC production. The chimeric human antibodies have a prolonged half-life and  
CC a reduced frequency of adverse effects when compared to mouse monoclonal  
CC antibodies

XX SQ Sequence 130 AA;

Query Match 100.0%; Score 624; DB 2; Length 130;  
Best Local Similarity 100.0%; Pred. No. 8.6e-51;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAFASHYAMSWVRQTPAKRLEWVAYISSGGSGTY 60  
Db 11 EVTLVESGGDFVKPGGSLKVSAAAGFAFASHYAMSWVRQTPAKRLEWVAYISSGGSGTY 70

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 119  
Db 71 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 129

RESULT 6  
AAB01627  
ID AAB01627 standard; protein; 130 AA.

XX AC AAB01627;

DT 07-DEC-2000 (first entry)

XX DE Murine immunoglobulin heavy chain variable region.

XX KW Mouse; immunoglobulin; H chain; heavy chain; variable region; cancer;  
XX humanised antibody.

XX OS Mus sp.

XX FH Key Location/Qualifiers  
FT Peptide 1..10  
FT /label= signal\_peptide  
FT Protein 11..130  
FT /label= mature\_immunoglobulin\_heavy\_chain\_variable region

XX PN EP1013761-A2.

XX PD 28-JUN-2000.

XX PF 18-SEP-1992; 99EP-00124345.

XX PR 18-SEP-1991; 91JP-00238375.

XX PR 18-SEP-1992; 92EP-00116026.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;

XX DR WPI; 2000-402204/35.

XX DR N-PSDB; AAA51003.

XX PT New humanized chimera antibody KM-871 useful for treating cancer,  
PT comprises variable region of mouse monoclonal antibody, reactive with  
PT ganglioside and human antibody constant region.

XX PS Claim 14; Page 27-28; 65pp; English.

XX CC The present sequence is a murine immunoglobulin heavy chain variable  
CC region from plasmid KM-641. The coding sequence was used in the creation  
CC of an expression vector, along with the sequence for a human antibody, to  
CC produce humanised chimaeric antibodies, which can be used to treat  
CC cancer. Humanised chimaeric antibodies are more effective than mouse  
CC antibodies as they do not provoke a reaction in the human and side  
CC effects, such as the formation of anti-mouse immunoglobulin antibody and  
CC the rapid half-life of the immunoglobulins, do not occur

XX SQ Sequence 130 AA;

Query Match 100.0%; Score 624; DB 3; Length 130;  
Best Local Similarity 100.0%; Pred. No. 8.6e-51;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAFASHYAMSWVRQTPAKRLEWVAYISSGGSGTY 60  
Db 11 EVTLVESGGDFVKPGGSLKVSAAAGFAFASHYAMSWVRQTPAKRLEWVAYISSGGSGTY 70

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 119  
Db 71 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 129

RESULT 7  
AAB81977  
ID AAB81977 standard; protein; 138 AA.

XX AC AAB81977;

DT 03-JUL-2001 (first entry)

XX DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 1.

XX KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
XX cancer.

XX OS Mus musculus.

XX PN WO200123432-A1.

XX PD 05-APR-2001.

XX PF 29-SEP-2000; 2000WO-JP006774.

XX PR 30-SEP-1999; 99JP-00278291.

XX PR 06-APR-2000; 2000JP-00105088.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Hanai N, Shitara K, Nakamura K, Niwa R;

XX DR WPI; 2001-266143/27.

XX PT New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.

XX PS Example 1; Page 138-139; 183pp; Japanese.

XX CC The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumours, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention

XX SQ Sequence 138 AA;

Query Match 100.0%; Score 624; DB 4; Length 138;  
Best Local Similarity 100.0%; Pred. No. 9.2e-51;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAFASHYAMSWVRQTPAKRLEWVAYISSGGSGTY 60  
Db 20 EVTLVESGGDFVKPGGSLKVSAAAGFAFASHYAMSWVRQTPAKRLEWVAYISSGGSGTY 79

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 119  
Db 80 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 138

RESULT 8  
ABU11002



ID ABU1002 standard; protein; 138 AA.  
XX AC ABU11002;  
XX XX  
DT 04-FEB-2003 (first entry)  
XX DE Modified ganglioside GD3 antibody associated protein #1.  
XX DE Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.  
XX KW Mus musculus.  
XX OS  
XX PN WO200278739-A1.  
XX PD 10-OCT-2002.  
XX PF 29-MAR-2002; 2002WO-JP003170.  
XX PR 29-MAR-2001; 2001JP-00097483.  
XX PR (KYOW ) KYOWA HAKKO KOGYO KK.  
XX PA Shitara K, Niwa R, Kanazawa J, Asada M;  
XX PI WPI; 2003-067410/06.  
XX DR  
XX PT Drugs containing genetically-modified antibody against ganglioside GD3,  
XX PT its fragment, immunocompetent cell activators or/and antitumor agents in  
XX PT combination, applicable in treating malignant tumor like melanoma.  
XX XX  
XX Example 3; Page 97; 121pp; Japanese.  
XX CC The invention describes drugs contain a genetically-modified antibody  
XX CC against ganglioside GD3 or its fragment and at least 1 of a substance  
XX CC capable of activating immunocompetent cells and a substance having an  
XX CC antitumor activity in combination. The drugs can be used to treat tumour  
XX CC like melanoma and can provide a treatment with enhanced therapeutic  
XX CC effect and little side-reactions, particularly to relieve problems of  
XX CC side-effects during the conventional single administration. This sequence  
XX CC represents a protein associated with the anti- ganglioside GD3 antibody  
XX SQ Sequence 138 AA;  
Query Match 100.0%; Score 624; DB 6; Length 138;  
Best Local Similarity 100.0%; Pred. No. 9.2e-51;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EVTLVESGGDFVKPGGSLKVS CAASGPAF SHYAMSWVRQTPAKRLEWVAYISSGGSTYY 60  
DB 20 EVTLVESGGDFVKPGGSLKVS CAASGPAF SHYAMSWVRQTPAKRLEWVAYISSGGSTYY 79  
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTYFYFDSWGQGTTLTVSS 119  
DB 80 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTYFYFDSWGQGTTLTVSS 138  
RESULT 9  
AAB81991  
ID AAB81991 standard; protein; 582 AA.  
XX AC AAB81991;  
XX XX  
DT 03-JUL-2001 (first entry)  
XX DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.  
XX DE Ganglioside; GD3; complementarity determining region; CDR; antibody;  
XX KW cancer.  
XX OS Synthetic.  
XX PN WO200123432-A1.  
XX PD  
XX PF  
XX PR 29-SEP-2000; 2000WO-JP005774.  
XX PR 30-SEP-1999; 99JP-00278291.  
XX PR 06-APR-2000; 2000JP-00105088.  
XX XX  
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX XX  
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX XX WPI; 2001-266143/27.  
XX DR  
XX PT New human type complementation-determining region-transplanted antibody  
XX PT and derivatives against ganglioside GD3, useful in diagnosis and therapy

PD 05-APR-2001.  
XX XX  
XX 29-SEP-2000; 2000WO-JP006774.  
XX XX  
XX 30-SEP-1999; 99JP-00278291.  
XX PR 06-APR-2000; 2000JP-00105088.  
XX XX  
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX XX  
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX XX WPI; 2001-266143/27.  
XX XX  
XX New human type complementation-determining region-transplanted antibody  
XX PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
XX PT of e.g. tumors with low antigenicity, little side effects but potent  
XX PT activity in cancer.  
XX XX  
XX Claim 39; Page 175-179; 183pp; Japanese.  
XX XX  
XX The present invention describes a monoclonal antibody which can react  
XX CC specifically with ganglioside GD3. The antibody and its derivatives are  
XX CC useful in the diagnosis and therapy of tumours, particularly cancer  
XX CC diagnosis. The present sequence is a protein used in the exemplification  
XX CC of the invention  
XX XX  
XX SQ Sequence 582 AA;  
Query Match 100.0%; Score 624; DB 4; Length 582;  
Best Local Similarity 100.0%; Pred. No. 4.4e-50;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EVTLVESGGDFVKPGGSLKVS CAASGPAF SHYAMSWVRQTPAKRLEWVAYISSGGSTYY 60  
DB 1 EVTLVESGGDFVKPGGSLKVS CAASGPAF SHYAMSWVRQTPAKRLEWVAYISSGGSTYY 60  
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTYFYFDSWGQGTTLTVSS 119  
DB 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTYFYFDSWGQGTTLTVSS 119  
RESULT 10  
AAB81985  
ID AAB81985 standard; protein; 119 AA.  
XX AC AAB81985;  
XX XX  
DT 03-JUL-2001 (first entry)  
XX DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 9.  
XX DE Ganglioside; GD3; complementarity determining region; CDR; antibody;  
XX KW cancer.  
XX OS Synthetic.  
XX PN WO200123432-A1.  
XX PD  
XX PF  
XX PR 29-SEP-2000; 2000WO-JP005774.  
XX PR 30-SEP-1999; 99JP-00278291.  
XX PR 06-APR-2000; 2000JP-00105088.  
XX XX  
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX XX  
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX XX WPI; 2001-266143/27.  
XX DR  
XX PT New human type complementation-determining region-transplanted antibody  
XX PT and derivatives against ganglioside GD3, useful in diagnosis and therapy

PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.

PS Claim 20; Page 142-143; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumours, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention

XX SQ Sequence 119 AA;

Query Match 92.8%; Score 579; DB 4; Length 119;

Best Local Similarity 91.6%; Pred. No. 1.3e-46;

Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 60

DB 1 EVQLVESGGDFVQPGGSLRVSCAASGFAF SHYAMSWVRQAPGKGLEWVAYISSGGSGTY 60

OY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTGYTFDSWGQGTLLTVSS 119

DB 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTGYTFDSWGQGTLLTVSS 119

RESULT 11

ABU11010

ID ABU11010 standard; protein; 119 AA.

XX AC ABU11010;

XX XX

DT 04-FEB-2003 (first entry)

XX Modified ganglioside GD3 antibody associated protein #3.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX OS Synthetic.

XX WO200278739-A1.

XX PD 10-OCT-2002.

XX PF 29-MAR-2002; 2002WO-JP003170.

XX PR 29-MAR-2001; 2001JP-00097483.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Shitara K, Niwa R, Kanazawa J, Asada M;

XX WPI; 2003-067410/06.

XX Drugs containing genetically-modified antibody against ganglioside GD3,  
PT its fragment, immunocompetent cell activators or/and anticancer agents in  
PT combination, applicable in treating malignant tumor like melanoma.

XX PS Claim 8; Page 99; 121pp; Japanese.

XX The invention describes drugs contain a genetically-modified antibody  
CC against ganglioside GD3 or its fragment and at least 1 of a substance  
CC capable of activating immunocompetent cells and a substance having an  
CC anticancer activity in combination. The drugs can be used to treat tumour  
CC like melanoma and can provide a treatment with enhanced therapeutic  
CC effect and little side-reactions, particularly to relieve problems of  
CC side-effects during the conventional single administration. This sequence  
CC represents a protein associated with the anti- ganglioside GD3 antibody

XX SQ Sequence 119 AA;

Query Match 92.8%; Score 579; DB 6; Length 119;

Best Local Similarity 91.6%; Pred. No. 1.3e-46;

Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 60

DB 1 EVQLVESGGDFVQPGGSLRVSCAASGFAF SHYAMSWVRQAPGKGLEWVAYISSGGSGTY 60

OY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTGYTFDSWGQGTLLTVSS 119

DB 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTGYTFDSWGQGTLLTVSS 119

RESULT 12

AA881987

ID AA881987 standard; protein; 582 AA.

XX AC AA881987;

XX DT 03-JUL-2001 (first entry)

XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.

XX Ganglioside; GD3; complementarity determining region; CDR; antibody;

XX cancer.

XX OS Synthetic.

XX WO200123432-A1.

XX PD 05-APR-2001.

XX PF 29-SEP-2000; 2000WO-JP006774.

XX PR 30-SEP-1999; 99JP-00278291.

XX PR 06-APR-2000; 2000JP-00105088.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Hanai N, Shitara K, Nakamura K, Niwa R;

XX WPI; 2001-266143/27.

XX New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.

XX PS Claim 41; Page 168-172; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumours, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention

XX SQ Sequence 582 AA;

Query Match 92.8%; Score 579; DB 4; Length 582;

Best Local Similarity 91.6%; Pred. No. 7.3e-46;

Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 60

DB 1 EVQLVESGGDFVQPGGSLRVSCAASGFAF SHYAMSWVRQAPGKGLEWVAYISSGGSGTY 60

OY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTGYTFDSWGQGTLLTVSS 119

DB 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTGYTFDSWGQGTLLTVSS 119

RESULT 13

AAW29994

ID AAW29994 standard; protein; 119 AA.

XX

AC AAW29994;  
 XX 25-MAR-2003 (revised)  
 DT 12-MAR-1998 (first entry)  
 XX Heavy chain variable region of MAb ior t1A.  
 DE  
 XX Heavy chain; variable region; monoclonal antibody; human; CD6; murine;  
 KW leukocyte differentiation antigen; hybridoma; humanisation; mutagenesis;  
 KW PCR; primer; amplification; inflammatory infiltration; skin; psoriasis;  
 KW diagnosis.  
 XX  
 OS Mus sp.  
 XX  
 XX WO9719111-A2.  
 PN  
 XX 29-MAY-1997.  
 XX  
 XX 18-NOV-1996; 96WO-CU000004.  
 PF  
 XX 17-NOV-1995; 95CU-00000120.  
 PR  
 XX (IMMU-) CENT IMMUNOLOGIA MOLECULAR.  
 PA  
 XX Montero Casimiro JE, Lombardero Valladares J, Perez Rodriguez R;  
 PI Sierra Blazquez P, Tormo Bravo BR;  
 PI  
 XX WPI; 1997-298060/27.  
 DR  
 XX Monoclonal antibody against human CD6 antigen - useful for diagnosis and  
 PT treatment of psoriasis.  
 PT  
 XX Claim 3; Page 27; 38pp; Spanish.  
 PS  
 XX This is the amino acid sequence of the heavy chain variable region of the  
 CC monoclonal antibody (MAb) ior t1A which recognises the human leukocyte  
 CC differentiation antigen CD6. The MAb is a murine IgG2-type Ab produced by  
 CC the usual hybridoma techniques. The coding sequence for the variable  
 CC region can be used to generate humanised variants, especially by  
 CC mutagenic PCR. CD6 has been shown to be expressed in T lymphocytes  
 CC involved in the inflammatory infiltration of the skin in psoriasis. The  
 CC anti-CD6 MAb can therefore be used to diagnose and treat psoriasis.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 119 AA;  
 Query Match 79.0%; Score 493; DB 2; Length 119;  
 Best Local Similarity 81.5%; Pred. No. 1.5e-38;  
 Matches 97; Conservative 3; Mismatches 19; Indels 0; Gaps 0;  
 QY 1 EVTLVESGGDFVKPGGSLKVCASGAFAPSHYAMSWVRQTPAKRLEWVAYISSGGSTYY 60  
 DB 1 EVQLVESGGGLVKPGGSLKLSCAASGFKFSRYAMSWVRQTPKRLWVATISSGGYIYY 60  
 QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMFYCTRVKLGTY--YFDSWGQGTTLTVSS 119  
 DB 61 PDSVKGRFTISRDNKNTLYLQMSLSRSDTAMFYCARRDYDLDYFDSWGQGTTLTVSS 119  
 RESULT 14  
 ABP60555  
 ID ABP60555 standard; protein; 134 AA.  
 XX  
 XX ABP60555;  
 AC  
 XX 21-MAR-2003 (first entry)  
 DT  
 XX Murine antibody 14F3 heavy chain variable region.  
 DE  
 XX Mouse; monoclonal antibody; 14F3; osteopathic; antirheumatic;  
 KW antiarthritic; antiinflammatory; cytostatic; antipsoriatic; antidiabetic;  
 KW neuroprotective; gene therapy; rheumatoid arthritis; osteoporosis;  
 KW bone cancer; osteolysis; osteoarthritis; immune disease; psoriasis;

KW insulin-dependent diabetes; inflammatory bowel disease;  
 KW multiple sclerosis; heavy chain variable region;  
 KW complementary determining region; CDR.  
 XX Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 KW Region 31..35  
 FT /label= CDR1  
 FT Region 50..66  
 FT /label= CDR2  
 FT Region 99..110  
 FT /label= CDR3  
 XX  
 XX WO200295012-A1.  
 PN  
 XX 28-NOV-2002.  
 PD  
 XX 03-MAY-2002; 2002WO-US014246.  
 PF  
 XX 18-MAY-2001; 2001US-0292031P.  
 PR  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 XX Sweet RW, Tornetta MA, Wattam TA;  
 PI  
 XX WPI; 2003-156758/15.  
 DR N-PSDB; ABV99887.  
 DR  
 XX New monoclonal antibody having the characteristics of a monoclonal  
 PT antibody 14F3, useful for treating or preventing osteopathic diseases,  
 PT e.g. rheumatoid arthritis, or osteoporosis, and immune diseases e.g.  
 PT psoriasis, or diabetes.  
 PT  
 XX Disclosure; Page 8; 51pp; English.  
 PS  
 XX The invention relates to a novel monoclonal antibody having the  
 CC identifying characteristics of, or that is a monoclonal antibody 14F3. An  
 CC antibody of the invention has osteopathic, antirheumatic, antiarthritic,  
 CC antiinflammatory, cytostatic, antipsoriatic, antidiabetic, and  
 CC neuroprotective activity. The polynucleotides encoding the antibodies of  
 CC the invention may have a use in gene therapy. The antibodies and  
 CC polypeptides are useful for treating or preventing osteopathic diseases,  
 CC such as rheumatoid arthritis, osteoporosis, metastatic and primary bone  
 CC cancer, wear debris induced osteolysis or osteoarthritis, and immune  
 CC diseases such as psoriasis, insulin-dependent diabetes, inflammatory  
 CC bowel disease or multiple sclerosis. The present sequence represents the  
 CC heavy chain variable region of the murine monoclonal antibody 14F3 of the  
 CC invention. The sequence contains three complementary determining regions  
 CC (CDR's)  
 XX  
 SQ Sequence 134 AA;  
 Query Match 78.0%; Score 487; DB 6; Length 134;  
 Best Local Similarity 79.3%; Pred. No. 6.3e-38;  
 Matches 96; Conservative 6; Mismatches 17; Indels 2; Gaps 1;  
 QY 1 EVTLVESGGDFVKPGGSLKVCASGAFAPSHYAMSWVRQTPAKRLEWVAYISSGGSTYY 60  
 DB 1 EVQLVESGGDLVKPGGSLKLSCAASGFTFSRYGMSWVRQTPDKRLEWVATISSGGSYTY 60  
 QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMFYCTRVKLGTY--YFDSWGQGTTLTVSS 118  
 DB 61 PDSVKGRFTISRDNKNTLYLQMSLSRSDTAMFYCARLDYGNRYRWYFDWGTGTTTVTS 120  
 QY 119 S 119  
 DB 121 S 121  
 RESULT 15  
 AAB20442



Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	624	100.0	130	4	US-09-225-322B-18	Sequence 18, Appl
2	624	100.0	130	4	US-09-764-304-18	Sequence 18, Appl
3	614	98.4	130	4	US-09-225-322B-8	Sequence 8, Appl
4	614	98.4	130	4	US-09-764-304-8	Sequence 8, Appl
5	493	79.0	119	4	US-08-875-674A-1	Sequence 1, Appl
6	486	77.9	247	5	PCR-US94-07659-2	Sequence 2, Appl
7	480	76.9	119	4	US-08-875-674A-3	Sequence 3, Appl
8	474	76.0	119	4	US-09-232-290-55	Sequence 55, Appl
9	472	75.6	239	2	US-08-553-497A-18	Sequence 18, Appl
10	469.5	75.2	135	3	US-08-579-378A-16	Sequence 16, Appl
11	466.5	74.8	118	1	US-08-326-363-2	Sequence 2, Appl
12	464	74.4	119	3	US-09-406-535-2	Sequence 2, Appl
13	460.5	73.8	124	4	US-09-518-737-2	Sequence 2, Appl
14	457.5	73.3	120	4	US-09-232-290-42	Sequence 42, Appl
15	457.5	73.3	456	4	US-09-495-880A-11	Sequence 11, Appl
16	457	73.2	217	5	PCR-US94-14106-59	Sequence 59, Appl
17	453	72.6	119	4	US-09-648-067A-15	Sequence 15, Appl
18	452	72.4	119	1	US-08-497-312-20	Sequence 20, Appl
19	450.5	72.2	120	2	US-07-934-373C-4	Sequence 4, Appl
20	450.5	72.2	120	3	US-08-437-642B-4	Sequence 4, Appl
21	450.5	72.2	120	4	US-08-146-206C-4	Sequence 4, Appl
22	450.5	72.2	120	4	US-09-705-686-4	Sequence 4, Appl
23	450.5	72.2	120	4	US-09-705-392A-4	Sequence 4, Appl
24	450.5	72.2	120	4	US-09-705-398-4	Sequence 4, Appl
25	450	72.1	119	2	US-08-475-000-16	Sequence 16, Appl
26	450	72.1	119	2	US-08-483-199-16	Sequence 16, Appl
27	450	72.1	119	2	US-08-484-508-16	Sequence 16, Appl

## ALIGNMENTS

```
RESULT 1
US-09-225-322B-18
; Sequence 18, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-225-322B-18
Query Match      100.0%; Score 624; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 9.5e-60;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  EVTLVESGGDFVKPGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
      |||
DB      11  EVTLVESGGDFVKPGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 70
      |||

QY      61  SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFFDSWGQGTTLTVSS 119
      |||
DB      71  SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFFDSWGQGTTLTVSS 129
      |||

RESULT 2
US-09-764-304-18
; Sequence 18, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER APPLICATION NUMBER: US 08/292,178

QY      1  EVTLVESGGDFVKPGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
      |||
DB      11  EVTLVESGGDFVKPGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 70
      |||

QY      61  SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFFDSWGQGTTLTVSS 119
      |||
DB      71  SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFFDSWGQGTTLTVSS 129
      |||

RESULT 2
US-09-764-304-18
; Sequence 18, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER APPLICATION NUMBER: US 08/292,178

QY      1  EVTLVESGGDFVKPGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
      |||
DB      11  EVTLVESGGDFVKPGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 70
      |||

QY      61  SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFFDSWGQGTTLTVSS 119
      |||
DB      71  SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFFDSWGQGTTLTVSS 129
      |||
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; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-18
Query Match      100.0%; Score 624; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 9.5e-60;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  EVTLVESGGDFVKPGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
      |||
DB      11  EVTLVESGGDFVKPGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 70
      |||

QY      61  SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFFDSWGQGTTLTVSS 119
      |||
DB      71  SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFFDSWGQGTTLTVSS 129
      |||

RESULT 3
US-09-225-322B-8
; Sequence 8, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-225-322B-8
Query Match      98.4%; Score 614; DB 4; Length 130;
Best Local Similarity 99.2%; Pred. No. 1.1e-58;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  EVTLVESGGDFVKPGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
      |||
DB      11  EVTLVESGGDFVKPGSLKVS CAASGFAF SHYAMSWVRQTPAKRLEWVAGISSGGSGTYY 70
      |||

QY      61  SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFFDSWGQGTTLTVSS 119
      |||
DB      71  SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFFDSWGQGTTLTVSS 129
      |||
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RESULT 4
US-09-764-304-8
; Sequence 8, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-8

Query Match          98.4%; Score 614; DB 4; Length 130;
Best Local Similarity 99.2%; Pred. No. 1.1e-58;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVTLVESGDDFVKPGGSLKVS CAASGFATSHYAMSVWRQTTPAKRLEWVAYISSGSGTYY 60
DB 11 EVTLVESGDDFVKPGGSLKVS CAASGFATSHYAMSVWRQTTPAKRLEWVAYISSGSGTYY 70
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 119
DB 71 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 129

RESULT 5
US-08-875-674A-1
; Sequence 1, Application US/08875674A
; Patent No. 6572857
; GENERAL INFORMATION:
; APPLICANT: MONTERO CASIMIRO, J. E.
; APPLICANT: LOMBARDERO VALLADARES, J.
; APPLICANT: P REZ RODR GUEZ, R.
; APPLICANT: SIERRA BL ZQUEZ, P.
; APPLICANT: TORMO BRAVO, B. R.
; TITLE OF INVENTION: Anti-CD6 monoclonal antibodies and their uses
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lackenbach Siegel Marzullo Aronson & Greenspan, P.C.
; STREET: One Chase Road
; CITY: Scarsdale
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10583
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk 3.5" (1.4 MB).
; COMPUTER: Compatible PC IBM (80486, 8 M Ram).
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; OPERATING SYSTEM: Windows 95.
; SOFTWARE: Word Perfect 5.0 for Windows 95.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,674A
; FILING DATE: 17-July-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/CU96/00004
; FILING DATE: 18-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: HENRY A. MARZULLO, JR.
; REGISTRATION NUMBER: 20,910
; REFERENCE/DOCKET NUMBER: P-12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 723-4300
; TELEFAX: (914)-723-4301
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 Amino acid residues.
; TYPE: Amino acid.
; STRANDEDNESS: Unknown.
; TOPOLOGY: Unknown.
; MOLECULE TYPE: Protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: -N Terminal fragment.
; ORIGINAL SOURCE:
; ORGANISM: Mice Balb/C
; INDIVIDUAL ISOLATE: ior t1a
; TISSUE TYPE: Murine hibridoma
; IMMEDIATE SOURCE:
; CLONE: Sub-clone ior t1a
; FEATURE:
; IDENTIFICATION METHOD: Experimental.
; OTHER INFORMATION: Sequence corresponding to the variable region
; Patent No. 6572857
; OTHER INFORMATION: of the heavy chain of the monoclonal antibody recognizing hum
; OTHER INFORMATION: designated as sub-clone ior t1a.
US-08-875-674A-1

Query Match          79.0%; Score 493; DB 4; Length 119;
Best Local Similarity 81.5%; Pred. No. 1.1e-45;
Matches 97; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 EVTLVESGDDFVKPGGSLKVS CAASGFATSHYAMSVWRQTTPAKRLEWVAYISSGSGTYY 60
DB 1 EVQLVESGGGLVKPGGSLKLS CAASGFKFSRYAMSVWRQTPEKRLWVATISSGSGTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 119
DB 61 PDSVKGRFTISRDNKNTLYLQWSSLSRSDTAMYYCARRDYDLDFDSWGQGTTLTVSS 119

RESULT 6
PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
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QY 61 SDSVKGRTISRDNKNTLYLQMSLSRSDSAMFYCTRVKLGTYYPDSWGQGTTLTVSS 119  
Db 61 PDTVKGRTISRDNKNTLYLQMSLSRSDTAYICTRYSSDPFFYFDYWGQGTTLTVSS 119

RESULT 9  
US-08-553-497A-18  
; Sequence 18, Application US/08553497A  
; Patent No. 5844093  
; GENERAL INFORMATION:  
; APPLICANT: KETTLERBOROUGH, C. A.  
; APPLICANT: BENDIG, MARY M.  
; APPLICANT: ANSELL, KEITH H.  
; APPLICANT: GUSSOW, DETLEF  
; APPLICANT: ADAN, JAUME  
; APPLICANT: MITJANS, FRANCESC  
; APPLICANT: ROSELL, ELISABET  
; APPLICANT: BLASCO, FRANCESC  
; APPLICANT: PIULATS, JAUME  
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
; STREET: 2200 CLARENDON BLVD. SUITE 1400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: US  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/553,497A  
; FILING DATE: 17-NOV-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/00978  
; FILING DATE: 16-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94104160.0  
; FILING DATE: 17-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94118970.6  
; FILING DATE: 02-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HAMLET-KING, DIANA  
; REGISTRATION NUMBER: 33,302  
; REFERENCE/DOCKET NUMBER: MERCK 1726  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-243-6333  
; TELEFAX: 703-243-6410  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 239 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-553-497A-18

Query Match 75.6%; Score 472; DB 2; Length 239;  
Best Local Similarity 77.3%; Pred. No. 4.8e-43;  
Matches 92; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAPSHYAMSVVROTPAKRLEWVAYISGGSGTYY 60  
Db 1 EVKLQESGDLVKPGGSLKLS CAASGFTFSYGVMSVVRQTPDKRLSVATISSGGAYIY 60

QY 61 SDSVKGRTISRDNKNTLYLQMSLSRSDSAMFYCTRVKLGTYYPDSWGQGTTLTVSS 119  
Db 61 PDTVKGRTISRDNKNTLYLQMSLSRSDTAYICTRYSSDPFFYFDYWGQGTTLTVSS 119

Db 61 PDSVKGRTISRDNKNTLYLQMSLSKSDTAMYYCARLETGYALDYWGQGTTLTVSS 119

RESULT 10  
US-08-579-378A-16  
; Sequence 16, Application US/08579378A  
; Patent No. 6210671  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: L-Selectin  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/579,378A  
; FILING DATE: 27-DEC-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/160,074  
; FILING DATE: 30-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/983,946  
; FILING DATE: 01-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95112895.8  
; FILING DATE: 17-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95114696.8  
; FILING DATE: 19-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Liebeschultz, Joe O.  
; REGISTRATION NUMBER: 37,505  
; REFERENCE/DOCKET NUMBER: 11823-002220  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 135 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-579-378A-16

Query Match 75.2%; Score 469.5; DB 3; Length 135;  
Best Local Similarity 79.8%; Pred. No. 4.4e-43;  
Matches 95; Conservative 6; Mismatches 15; Indels 3; Gaps 2;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAPSHYAMSVVROTPAKRLEWVAYISGGSGTYY 60  
Db 20 EVKLVESGGDLVKPGGSLKLS CAASGFTFSYGVMSVVRQTPDKRLSVATISSGGSGTYY 78

QY 61 PDSVKGRTISRDNKNTLYLQMSLSRSDSAMFYCTRVKLGTYYPDSWGQGTTLTVSS 119  
Db 79 PDSVKGRTISRDNKNTLYLQMSLSRSDTAMYYCARDYDG--YFDYWGQGTTLTVSS 135

RESULT 11  
US-08-326-362-2  
; Sequence 2, Application US/08326362  
; Patent No. 5730981  
; GENERAL INFORMATION:

APPLICANT: Bosslet, Klaus  
APPLICANT: Seeman, Gerhard  
APPLICANT: Dippold, Wolfgang  
TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,  
TITLE OF INVENTION: Its Preparation and Use as a Tumortherapeutic Agent  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/326,362  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/032,863  
FILING DATE: 17-MAR-1993  
APPLICATION NUMBER: DE P 42 08 795.3  
FILING DATE: 19-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Einaudi, Carol P.  
REGISTRATION NUMBER: 32,220  
REFERENCE/DOCKET NUMBER: 02481-1276-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-326-362-2

Query Match 74.8%; Score 466.5; DB 1; Length 118;  
Best Local Similarity 77.3%; Pred. No. 7.9e-43;  
Matches 92; Conservative 7; Mismatches 19; Indels 1; Gaps 1;  
Qy 1 EVTLVESGGDFVKPGGSLKVCASGAFSHYAMSWVRQTPAKRLEWVAYISGGSGTYY 60  
Db 1 QVQLQSGGGLVKPGGSLTSCAASRFTFTSYAMSWVRQTPAKRLEWVAYISGGASTYY 60  
Qy 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTYVDFDSWGQGTTLTVSS 119  
Db 61 RDSVKGRFTISRDNKNTLYLQMSLRSEDTAMYICARGG-SRYANDYWGQGTTLTVSS 118

RESULT 12  
US-09-406-535-2  
Sequence 2, Application US/09406535  
Patent No. 6376653  
GENERAL INFORMATION:  
APPLICANT: Connie L. Erickson-Miller  
APPLICANT: Stephen D. Holmes  
APPLICANT: James D. Winkler  
TITLE OF INVENTION: Tie2 Antagonist Antibodies  
FILE REFERENCE: P50844  
CURRENT APPLICATION NUMBER: US/09/406,535  
CURRENT FILING DATE: 1999-09-27  
EARLIER APPLICATION NUMBER: 60/102,100  
EARLIER FILING DATE: 1998-09-28  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2

LENGTH: 119  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-406-535-2  
Query Match 74.4%; Score 464; DB 3; Length 119;  
Best Local Similarity 74.8%; Pred. No. 1.5e-42;  
Matches 89; Conservative 8; Mismatches 22; Indels 0; Gaps 0;  
Qy 1 EVTLVESGGDFVKPGGSLKVCASGAFSHYAMSWVRQTPAKRLEWVAYISGGSGTYY 60  
Db 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSDYGMHVRQAPEKGLWEVAYINSGSTITY 60  
Qy 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTYVDFDSWGQGTTLTVSS 119  
Db 61 ADTVKGRFTISRDNKNTLYLQMSLRSEDTAIYICARGYGPYFFDWGGTALTUSS 119  
RESULT 13  
US-09-518-737-2  
Sequence 2, Application US/09518737  
Patent No. 6709833  
GENERAL INFORMATION:  
APPLICANT: FUKUI, YASUHIKA  
APPLICANT: NAGATA, SATOSHI  
APPLICANT: SHIRAI, RYUICHI  
APPLICANT: SAITO, NAOAKI  
TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING  
FILE REFERENCE: 1965/49618  
CURRENT APPLICATION NUMBER: US/09/518,737  
CURRENT FILING DATE: 2000-03-03  
PRIOR APPLICATION NUMBER: JP 1999-250209  
PRIOR FILING DATE: 1999-09-03  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 124  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-518-737-2

Query Match 73.8%; Score 460.5; DB 4; Length 124;  
Best Local Similarity 74.8%; Pred. No. 3.7e-42;  
Matches 92; Conservative 7; Mismatches 17; Indels 7; Gaps 2;  
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Db 1 EVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMASWARQTPDKRLEWVASISGGSGTYY 60  
Qy 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTR- ---VKLGTYVDFDSWGQGTTLT 116  
Db 61 PDSVKGRFTISRDNKNTLYLQMSLRSEDTAMYICARQRYVNFGIAY- ---WGQGTTLT 117  
Qy 117 VSS 119  
Db 118 VSA 120

RESULT 14  
US-09-232-290-42  
Sequence 42, Application US/09232290A  
Patent No. 6815540  
GENERAL INFORMATION:  
APPLICANT: PLUCKTHUN, ANDREAS  
APPLICANT: NIEBA, LARS  
APPLICANT: HONEGGER, ANNEMARIE  
TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH  
TITLE OF INVENTION: INCREASED SOLUBILITY  
FILE REFERENCE: MORPHO/7  
CURRENT APPLICATION NUMBER: US/09/232,290A  
CURRENT FILING DATE: 1999-01-15  
EARLIER APPLICATION NUMBER: PCT/EP96/02230

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; EARLIER FILING DATE: 1996-05-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 120
; TYPE: PRN
; ORGANISM: Murine
US-09-232-290-42

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		Query Match	73.3%	Score 457.5;	DB 4; Length 120;
		Best Local Similarity	75.8%;	Pred. No. 7.5e-42;	
		Matches	91; Conservative	8; Mismatches 20; Indels 1; Gaps 1;	
Qy	1	EVTLVESGGDFVPGGSLVKSCAASGFAPSHYAMSWVRQTTPAKRLEWVAIVSSGGSTYY	60		
Dd	1	EVTLVESGGDLVPKGGSKLSCAASGPSFSGYSMSWRQTDPDKRELVATISNGGYTYY	60		
Qy	61	SDSVKGRTFTSRDNAGNTLYLOWRSLSSESAMYFCT-RVKLGITYTYFDSVGCGTTLTUVSS	119		
Dd	61	PDSPVGRTFTSRDNAGNTLYLOWSSLKSSEDSAMYTCARRERYDENGFAFYQGGLTVTSA	120		

**RESULT 15**

```

US-09-495-880A-11
; Sequence 11, Application US/09495880A
; Patent No. 6667150
; GENERAL INFORMATION:
; APPLICANT: RUDERT, FRITZ
; APPLICANT: GE, LIMING
; APPLICANT: ILIAG, VIC
; TITLE OF INVENTION: NOVEL METHOD AND PHASE FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING MEMBERS OF A MULTIMERIC
; TITLE OF INVENTION: (POLY)PEPTIDE COMPLEX
; FILE REFERENCE: MORPHO/9
; CURRENT APPLICATION NUMBER: US/09/495, 880A
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: PCT/EP98/04836
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: EP 97 11 3319.4
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ompA-FLAG-scFv (anti-
; -OTHER INFORMATION: HAG)-gene IIIs encoded by phage vector fhaG1A (circular
US-09-495-880A-11

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Query Match	73.3%	Score	457.5;	DB	4;	Length	456;
Best Local Similarity Matches	91;	Conservative	8;	Mismatches	20;	Indels	1; Gaps 1;
Qy	1	EVTLVSGGDFVKPGSLKLVSCAASGFAPSHYAMSWVRQTPAKRLEWAVISSGGSGTTY	60				
Db	170	EVQLVESGGDLVFKPGSKLSCAASGSFSSYGMSWRQTDPDKRLEWATISNGGGVTTY	229				
Qy	61	SDSVKGRFTISRDNAKNTLYLQWRSIRSEDSAMYFCT-RVKLTGYTFDSHGQDTTLTVSS	119				
Db	230	PDSVKGRFTISRDNAKNTLYLQWSSLKESDAMYCYCARRERYDENGFAFYMGQCTLTVSA	289				

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Job time : 10.0342 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 1, 2005, 09:02:01 ; Search time 31.3976 Seconds  
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Title: US-10-089-500-55

Perfect score: 624

Sequence: 1 EVTLVSGGDFVKPGSLKV.....KLGTYFDSWGQGTTLTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications\_AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	624	100.0	130	14	US-10-265-713-18
3	624	100.0	130	14	US-10-166-626-18
4	614	98.4	130	9	US-09-764-304-8
5	614	98.4	130	14	US-10-265-713-8
6	614	98.4	130	14	US-10-166-626-8
7	487	78.0	134	16	US-10-477-377-3
8	486	77.9	140	13	US-10-006-773-4
9	481	77.1	121	15	US-10-276-939-3
10	477	76.4	232	18	US-10-511-794-17
11	477	76.4	241	18	US-10-511-794-16
12	477	76.4	241	18	US-10-511-794-21
13	475	76.1	119	14	US-10-281-479A-61
14	475	76.1	119	14	US-10-275-180A-61
15	475	76.1	119	14	US-10-286-132A-61
16	475	76.1	119	14	US-10-281-479A-23
17	475	76.1	119	14	US-10-286-132A-23
18	473.5	75.9	120	15	US-10-275-180A-23
19	473.5	75.9	120	15	US-10-412-406-2
20	473.5	75.9	120	15	US-10-412-406-33
21	473	75.8	123	9	US-09-144-886-61
22	473	75.8	123	16	US-10-632-706-58
23	472	75.6	731	20	US-11-035-599-51
24	471	75.5	119	14	US-10-270-071-5
25	471	75.5	119	14	US-10-270-071-6
26	471	75.5	262	14	US-10-270-071-20
27	471	75.5	262	14	US-10-270-071-24
28	471	75.5	262	14	US-10-270-071-28
29	471	75.5	268	14	US-10-270-071-10
30	471	75.5	268	14	US-10-270-071-12
31	471	75.5	268	14	US-10-270-071-14
32	471	75.5	268	14	US-10-270-071-16
33	471	75.5	415	14	US-10-328-190-12
34	469	75.2	262	14	US-10-270-071-34
35	469	75.2	268	14	US-10-270-071-32
36	469	75.2	268	14	US-10-328-190-2
37	469	75.2	268	14	US-10-328-190-4
38	469	75.2	364	17	US-10-829-388-11
39	469	75.2	370	17	US-10-829-388-1
40	468.5	75.1	118	9	US-09-423-800-46
41	468.5	75.1	118	14	US-10-182-018-46
42	468.5	75.1	118	14	US-10-169-003-46
43	468.5	75.1	118	14	US-10-337-981-46
44	468.5	75.1	118	15	US-10-344-733-46
45	468.5	75.1	118	20	US-11-047-996-46
46	468.5	75.1	118	20	US-11-047-996-88
47	468.5	75.1	137	9	US-09-423-800-76
48	468.5	75.1	137	14	US-10-337-981-76
49	468.5	75.1	137	11	US-09-910-358D-4
50	468	75.0	125	11	US-09-910-358D-8
51	468	75.0	140	9	US-09-286-240-4
52	468	75.0	144	9	US-09-881-823-12
53	468	75.0	155	14	US-10-077-624-7
54	468	75.0	155	16	US-10-706-391-4
55	468	75.0	165	14	US-10-077-624-4
56	468	75.0	165	16	US-10-706-391-2
57	468	75.0	158	15	US-10-226-785-32
58	467	74.8	115	15	US-10-436-782-37
59	466	74.7	115	15	US-10-436-783-5
60	466	74.7	115	18	US-10-994-129-5
61	466	74.7	115	20	US-11-004-795A-37
62	466	74.7	115	20	US-11-004-794A-37
63	466	74.7	120	15	US-10-412-406-10
64	465.5	74.6	120	15	US-10-490-535-2
65	462	74.0	123	17	US-10-412-406-14
66	461.5	74.0	120	15	US-09-518-737-2
67	460.5	73.8	124	17	US-10-723-748-2
68	460.5	73.6	120	18	US-10-995-316-200
69	459	73.6	116	14	US-10-169-351-47
70	458.5	73.5	118	15	US-10-474-832-2
71	458.5	73.5	118	15	US-10-474-832-20
72	458.5	73.3	456	15	US-09-144-886-11
73	457	73.2	123	9	US-09-144-886-60
74	457	73.2	123	16	US-10-632-706-57
75	457	73.2	123	15	US-10-412-406-12
76	456.5	73.2	120	15	US-10-412-406-16
77	456.5	73.2	663	15	US-10-412-406-32
78	456.5	73.2	117	14	US-10-328-190-8
79	455	72.9	120	9	US-09-229-200A-6
80	454.5	72.8	119	14	US-10-044-896-6
81	454	72.8	136	17	US-10-910-901-24
82	454	72.8	119	9	US-09-811-123-3
83	453	72.6	119	14	US-10-268-501-6
84	453	72.6	119	14	US-10-268-501-6

Sequence 21, Appl  
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Sequence 61, Appl  
Sequence 61, Appl  
Sequence 23, Appl  
Sequence 23, Appl  
Sequence 23, Appl  
Sequence 33, Appl  
Sequence 33, Appl  
Sequence 58, Appl  
Sequence 51, Appl  
Sequence 5, Appl  
Sequence 6, Appl  
Sequence 20, Appl  
Sequence 28, Appl  
Sequence 10, Appl  
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Sequence 14, Appl  
Sequence 16, Appl  
Sequence 12, Appl  
Sequence 34, Appl  
Sequence 32, Appl  
Sequence 2, Appl  
Sequence 4, Appl  
Sequence 11, Appl  
Sequence 1, Appl  
Sequence 46, Appl  
Sequence 46, Appl  
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Sequence 88, Appl  
Sequence 76, Appl  
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Sequence 8, Appl  
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Sequence 4, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 32, Appl  
Sequence 37, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 37, Appl  
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Sequence 2, Appl  
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Sequence 47, Appl  
Sequence 2, Appl  
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Sequence 11, Appl  
Sequence 60, Appl  
Sequence 57, Appl  
Sequence 12, Appl  
Sequence 16, Appl  
Sequence 32, Appl  
Sequence 8, Appl  
Sequence 6, Appl  
Sequence 6, Appl  
Sequence 24, Appl  
Sequence 3, Appl  
Sequence 6, Appl

85 453 72.6 119 15 US-10-608-626-6 Sequence 6, Appli  
86 453 72.6 119 15 US-10-600-152-15 Sequence 15, Appl  
87 453 72.6 119 16 US-10-619-754-6 Sequence 6, Appli  
88 453 72.6 119 16 US-10-719-310-6 Sequence 6, Appli  
89 453 72.6 119 17 US-10-861-049-42 Sequence 42, Appl  
90 453 72.6 120 17 US-10-938-353-104 Sequence 104, App  
91 453 72.6 121 15 US-10-447-331-4 Sequence 4, Appli  
92 453 72.6 269 13 US-10-027-770-2 Sequence 2, Appli  
93 452 72.4 119 14 US-10-281-479A-60 Sequence 60, Appl  
94 452 72.4 119 14 US-10-275-180A-60 Sequence 60, Appl  
95 452 72.4 119 14 US-10-286-132A-60 Sequence 60, Appl  
96 452 72.4 269 13 US-10-027-770-5 Sequence 5, Appli  
97 452 72.4 451 16 US-10-679-620-78 Sequence 78, Appl  
98 452 72.4 512 16 US-10-679-620-70 Sequence 70, Appl  
99 452 72.4 517 16 US-10-679-620-68 Sequence 68, Appl  
100 452 72.4 519 16 US-10-679-620-66 Sequence 66, Appl

## ALIGNMENTS

## RESULT 1

US-09-764-304-18  
; Sequence 18, Application US/09764304  
; Patent No. US20020026036A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/764,304  
; EARLIER FILING DATE: 2001-01-19  
; EARLIER APPLICATION NUMBER: 09/225,322  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER APPLICATION NUMBER: US 08/454,680  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER APPLICATION NUMBER: US 08/408,133  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER APPLICATION NUMBER: US 08/292,178  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; EARLIER FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: cDNA KM-641  
US-09-764-304-18  
Query Match 100.0%; Score 624; DB 9; Length 130;  
Best Local Similarity 100.0%; Pred. No. 2.8e-50;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EYTLVESGGDFVKPGGSLKSCAAGFAFHYAMSWVRQTPAKRLEWYAYISGGSGGY 60  
DB 11 EYTLVESGGDFVKPGGSLKSCAAGFAFHYAMSWVRQTPAKRLEWYAYISGGSGGY 70  
QY 61 SDSVKGRTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLTGYTFDSWGQGTTLTVSS 119  
DB 71 SDSVKGRTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLTGYTFDSWGQGTTLTVSS 129

## RESULT 2

US-10-265-713-18  
; Sequence 18, Application US/10265713  
; Patent No. US20030166876A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/10/166,626  
; EARLIER FILING DATE: 2002-06-12  
; EARLIER APPLICATION NUMBER: US/09/225,322B  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER APPLICATION NUMBER: US 08/454,680  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER APPLICATION NUMBER: US 08/408,133  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER APPLICATION NUMBER: US 08/292,178  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; EARLIER FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: cDNA KM-641  
US-10-265-713-18  
Query Match 100.0%; Score 624; DB 9; Length 130;  
Best Local Similarity 100.0%; Pred. No. 2.8e-50;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EYTLVESGGDFVKPGGSLKSCAAGFAFHYAMSWVRQTPAKRLEWYAYISGGSGGY 60  
DB 11 EYTLVESGGDFVKPGGSLKSCAAGFAFHYAMSWVRQTPAKRLEWYAYISGGSGGY 70  
QY 61 SDSVKGRTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLTGYTFDSWGQGTTLTVSS 119  
DB 71 SDSVKGRTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLTGYTFDSWGQGTTLTVSS 129

## RESULT 3

US-10-166-626-18  
; Sequence 18, Application US/10166626  
; Patent No. US20030166876A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/10/166,626  
; EARLIER FILING DATE: 2002-06-12  
; EARLIER APPLICATION NUMBER: US/09/225,322B  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER APPLICATION NUMBER: US 08/454,680  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER APPLICATION NUMBER: US 08/408,133  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER APPLICATION NUMBER: US 08/292,178  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; EARLIER FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641  
US-10-265-713-18  
Query Match 100.0%; Score 624; DB 14; Length 130;  
Best Local Similarity 100.0%; Pred. No. 2.8e-50;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EYTLVESGGDFVKPGGSLKSCAAGFAFHYAMSWVRQTPAKRLEWYAYISGGSGGY 60  
DB 11 EYTLVESGGDFVKPGGSLKSCAAGFAFHYAMSWVRQTPAKRLEWYAYISGGSGGY 70  
QY 61 SDSVKGRTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLTGYTFDSWGQGTTLTVSS 119  
DB 71 SDSVKGRTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLTGYTFDSWGQGTTLTVSS 129

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-18

Query Match      100.0%; Score 624; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.8e-50;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSVWRQTPAKRLEWVAYISSGGSGTYY 60
   |||||
Db 11 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSVWRQTPAKRLEWVAYISSGGSGTYY 70
   |||||

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 119
   |||||
Db 71 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 129
   |||||

RESULT 4
US-09-764-304-8
; Sequence 8, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; PRIOR FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-764-304-8

Query Match      98.4%; Score 614; DB 9; Length 130;
Best Local Similarity 99.2%; Pred. No. 2.3e-49;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSVWRQTPAKRLEWVAYISSGGSGTYY 60
   |||||
Db 11 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSVWRQTPAKRLEWVAYISSGGSGTYY 70
   |||||

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 119
   |||||
Db 71 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 129
   |||||

RESULT 5
US-10-265-713-8
; Sequence 8, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-8

Query Match      98.4%; Score 614; DB 14; Length 130;
Best Local Similarity 99.2%; Pred. No. 2.3e-49;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSVWRQTPAKRLEWVAYISSGGSGTYY 60
   |||||
Db 11 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSVWRQTPAKRLEWVAYISSGGSGTYY 70
   |||||

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 119
   |||||
Db 71 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 129
   |||||

RESULT 6
US-10-166-626-8
; Sequence 8, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-03-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
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; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-8

Query Match
Best Local Similarity 98.4%; Score 614; DB 14; Length 130;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTTPAKRLEWVAYISSGGSGTY 60
DB 11 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTTPAKRLEWVAGISSGGSGTY 70
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTY YFDSWGQGTTLTVSS 119
DB 71 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTY YFDSWGQGTTLTVSS 129

RESULT 7
US-10-477-377-3
; Sequence 3, Application US/10477377
; Publication No. US20040213788A1
; GENERAL INFORMATION:
; APPLICANT: Sweet, Raymond
; APPLICANT: Tornetta, Mark
; APPLICANT: Wattam, Trevor
; TITLE OF INVENTION: Anti-RANK Ligand Monoclonal Antibodies
; FILE REFERENCE: GP50050
; CURRENT APPLICATION NUMBER: US/10/477,377
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US02/14246
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 60/292,031
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-477-377-3

Query Match
Best Local Similarity 78.0%; Score 487; DB 16; Length 134;
Matches 96; Conservative 6; Mismatches 17; Indels 2; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTTPAKRLEWVAYISSGGSGTY 60
DB 1 EVQLVESGDDLVPKPGGSLKLS CAASGFTFSRYGMSWVRQTPDKRLEWVATISSGGSYTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 118
DB 61 PDSVKGRFTISRDNKNTLYLQMRSLKSEDTAMYCARLDGYNRYRWYFDVWGTTTVTS 120
QY 119 $ 119
DB 121 $ 121

RESULT 8
US-10-006-773-4
; Sequence 4, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
; FILE REFERENCE: 003
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; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-4

Query Match
Best Local Similarity 77.9%; Score 486; DB 13; Length 140;
Matches 94; Conservative 9; Mismatches 16; Indels 2; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTTPAKRLEWVAYISSGGSGTY 60
DB 20 EVVVESGGDFVKPGGSLKLS CAAGFTFSRYAMSWVRQTPDKRLEWVATISSGGSHY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTR--VKLGTYYFDSWGQGTTLTVS 118
DB 80 PDSVKGRFTISRDNKNTLYLQMRSLRSEDTAIYCARPGYDRGAWFFDVWGAGTTTVTS 139
QY 119 $ 119
DB 140 $ 140

RESULT 9
US-10-276-939-3
; Sequence 3, Application US/10276939
; Publication No. US20030215450A1
; GENERAL INFORMATION:
; APPLICANT: BLAKE, SIMON M.
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TAYLOR, ALEXANDER H.
; APPLICANT: WATTAM, TREVOR A.
; TITLE OF INVENTION: Anti-RANK Ligand Monoclonal Antibodies
; FILE REFERENCE: GP50024
; CURRENT APPLICATION NUMBER: US/10/276,939
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: PCT/US01/16865
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,628
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Murine
US-10-276-939-3

Query Match
Best Local Similarity 77.1%; Score 481; DB 15; Length 121;
Matches 95; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF SHYAMSWVRQTTPAKRLEWVAYISSGGSGTY 60
DB 1 EVQLVESGDDLVPKPGGSLKLS CAASGFTFSRYGMSWVRQTPDKRLEWVATISSGGSIY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 118
DB 61 PDSVKGRFTISRDNKNTLYLQMRSLKSEDTAMYCARLDGYNRYRWYFDVWGTTTVTS 120
QY 119 $ 119
DB 121 $ 121

RESULT 10
```



```
US-10-511-794-17
; Sequence 17, Application US/10511794
; Publication No. US20050158322A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: ANTIBODY FRAGMENTS SPECIFIC FOR HUMAN CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN (CEA)
; FILE REFERENCE: 976-20 PCT/US
; CURRENT APPLICATION NUMBER: US/10/511.794
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/CU2003/000005
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: CU2002/0086
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: diabody
US-10-511-794-17

Query Match          76.4%; Score 477; DB 18; Length 232;
Best Local Similarity 79.2%; Pred. No. 2.3e-36;
Matches 95; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

QY 1 EVTLVSGGDFVKPGGSLKVS CAASGFAPFSHYAMSWVROTPAKRLEWVAIISGGSGTYY 60
   |||||
DB 1 EVKLVESGGDLVKPGGSLKVS CAASGFAPFSHYAMSWVROTPEKRLEWVAFISDGI-AYY 59
   |||||

QY 61 SDSVKGRFTISRDNARKNTLYLQMRSLRSDSAMYFCTRV-KLGTYYFDSNGQGTTLTVSS 119
   :|||
DB 60 ADSVKGRFTISRDNARNILYLQMSLSRSEDAMYCARVYVYSSYFDYWGQGTTLTVSS 119

RESULT 11
US-10-511-794-16
; Sequence 16, Application US/10511794
; Publication No. US20050158322A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: ANTIBODY FRAGMENTS SPECIFIC FOR HUMAN CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN (CEA)
; FILE REFERENCE: 976-20 PCT/US
; CURRENT APPLICATION NUMBER: US/10/511.794
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/CU2003/000005
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: CU2002/0086
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv
US-10-511-794-16

Query Match          76.4%; Score 477; DB 18; Length 241;
Best Local Similarity 79.2%; Pred. No. 2.4e-36;
Matches 95; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

QY 1 EVTLVSGGDFVKPGGSLKVS CAASGFAPFSHYAMSWVROTPAKRLEWVAIISGGSGTYY 60
   |||||
DB 1 EVKLVESGGDLVKPGGSLKVS CAASGFAPFSHYAMSWVROTPEKRLEWVAFISDGI-AYY 59
   |||||

QY 61 SDSVKGRFTISRDNARKNTLYLQMRSLRSDSAMYFCTRV-KLGTYYFDSNGQGTTLTVSS 119
   :|||
DB 60 ADSVKGRFTISRDNARNILYLQMSLSRSEDAMYCARVYVYSSYFDYWGQGTTLTVSS 119
```

## RESULT 12

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US-10-511-794-21
; Sequence 21, Application US/10511794
; Publication No. US20050158322A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: ANTIBODY FRAGMENTS SPECIFIC FOR HUMAN CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN (CEA)
; FILE REFERENCE: 976-20 PCT/US
; CURRENT APPLICATION NUMBER: US/10/511.794
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/CU2003/000005
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: CU2002/0086
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: diabody MS
US-10-511-794-21
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```
Query Match          76.4%; Score 477; DB 18; Length 255;
Best Local Similarity 79.2%; Pred. No. 2.5e-36;
Matches 95; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

QY 1 EVTLVSGGDFVKPGGSLKVS CAASGFAPFSHYAMSWVROTPAKRLEWVAIISGGSGTYY 60
   |||||
DB 1 EVKLVESGGDLVKPGGSLKVS CAASGFAPFSHYAMSWVROTPEKRLEWVAFISDGI-AYY 59
   |||||

QY 61 SDSVKGRFTISRDNARKNTLYLQMRSLRSDSAMYFCTRV-KLGTYYFDSNGQGTTLTVSS 119
   :|||
DB 60 ADSVKGRFTISRDNARNILYLQMSLSRSEDAMYCARVYVYSSYFDYWGQGTTLTVSS 119
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## RESULT 13

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US-10-281-479A-61
; Sequence 61, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERE
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 21085.002906
; CURRENT APPLICATION NUMBER: US/10/281.479A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/391.478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346.402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201.344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 119
; TYPE: PRT
; ORGANISM: artificial sequence
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; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthetic  
US-10-281-479A-61

Query Match 76.1%; Score 475; DB 14; Length 119;  
Best Local Similarity 79.8%; Pred. No. 1.7e-36;  
Matches 95; Conservative 3; Mismatches 21; Indels 0; Gaps 0;  
  
QY 1 EYTLVESGGDFVKPGGSLKVSAAAGFAPSHYAMSWVRQTPAKRLEWVAYISSGGSGTY 60  
Db 1 EYMLVESGGGLVKPGGSLKLSAAAGFTFSSYVMSWVRQTPKRLWVATISSGGSYTY 60  
  
QY 61 SDSVKGRTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTYFYFDSWGQGTTLTVSS 119  
Db 61 PDSVKGRTISRDNKNTLYLQMSLRSEDTAMYICARRGDSMITTDYWGQGTTLTVSS 119

RESULT 14  
US-10-275-180A-61  
; Sequence 61, Application US/10275180A  
; Publication No. US20030190687A1  
; GENERAL INFORMATION:  
; APPLICANT: The UAB Research Foundation  
; APPLICANT: Zhou, Tong  
; APPLICANT: Ichikawa, Kimihisa  
; APPLICANT: Kimberly, Robert P.  
; APPLICANT: Koopman, William J.  
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSIS  
; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF  
; FILE REFERENCE: 21085.0029U5  
; CURRENT APPLICATION NUMBER: US/10/275,180A  
; CURRENT FILING DATE: 2002-10-31  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 61  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e = Synthetic Construct  
US-10-275-180A-61

Query Match 76.1%; Score 475; DB 14; Length 119;  
Best Local Similarity 79.8%; Pred. No. 1.7e-36;  
Matches 95; Conservative 3; Mismatches 21; Indels 0; Gaps 0;  
  
QY 1 EYTLVESGGDFVKPGGSLKVSAAAGFAPSHYAMSWVRQTPAKRLEWVAYISSGGSGTY 60  
Db 1 EYMLVESGGGLVKPGGSLKLSAAAGFTFSSYVMSWVRQTPKRLWVATISSGGSYTY 60  
  
QY 61 SDSVKGRTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTYFYFDSWGQGTTLTVSS 119  
Db 61 PDSVKGRTISRDNKNTLYLQMSLRSEDTAMYICARRGDSMITTDYWGQGTTLTVSS 119

RESULT 15  
US-10-286-132A-61  
; Sequence 61, Application US/10286132A  
; Publication No. US20030198637A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhou, Tong  
; APPLICANT: Kimberly, Robert P.  
; APPLICANT: Koopman, William J.  
; APPLICANT: LoBuglio, Albert S.  
; APPLICANT: Buchsbaum, Donald J.  
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF  
; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF  
; FILE REFERENCE: 21085.0029U7  
; CURRENT APPLICATION NUMBER: US/10/286,132A  
; CURRENT FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: US 60/346,402  
; PRIOR FILING DATE: 2001-11-01

; PRIOR APPLICATION NUMBER: PCT/US01/14151  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/201,344  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 61  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthetic  
US-10-286-132A-61

Query Match 76.1%; Score 475; DB 14; Length 119;  
Best Local Similarity 79.8%; Pred. No. 1.7e-36;  
Matches 95; Conservative 3; Mismatches 21; Indels 0; Gaps 0;  
  
QY 1 EYTLVESGGDFVKPGGSLKVSAAAGFAPSHYAMSWVRQTPAKRLEWVAYISSGGSGTY 60  
Db 1 EYMLVESGGGLVKPGGSLKLSAAAGFTFSSYVMSWVRQTPKRLWVATISSGGSYTY 60  
  
QY 61 SDSVKGRTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTYFYFDSWGQGTTLTVSS 119  
Db 61 PDSVKGRTISRDNKNTLYLQMSLRSEDTAMYICARRGDSMITTDYWGQGTTLTVSS 119

Search completed: August 1, 2005, 09:28:03  
Job time : 32.3976 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 1, 2005, 08:58:15 ; Search time 6.73864 Seconds  
(without alignments)  
1699.125 Million cell updates/sec

Title: US-10-089-500-55

Perfect score: 624

Sequence: 1 EVTLVSGGDFVKPGSLKV.....KLGTYYFDSNGQGTTLTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	479	76.8	119	2 B34353	anti-peptide Fab'
2	471	75.5	120	2 S55316	Ig heavy chain V r
3	470.5	75.4	121	2 I27887	Ig heavy chain V r
4	469	75.2	120	2 S55337	Ig heavy chain V r
5	469	75.2	122	2 E27888	Ig heavy chain V r
6	467	74.8	111	2 PH1007	Ig heavy chain V r
7	466.5	74.8	119	2 F27888	Ig heavy chain V r
8	464	74.4	138	2 S09258	Ig heavy chain V r
9	463	74.2	120	2 S55339	Ig heavy chain V r
10	462.5	74.1	118	2 PH0097	Ig heavy chain V r
11	462	74.0	118	2 S20641	Ig heavy chain V r
12	461	73.9	117	2 PL0249	Ig heavy chain V r
13	460	73.7	120	2 S55338	Ig heavy chain V r
14	457.5	73.3	254	2 B31790	Ig heavy chain V r
15	456.5	73.2	118	2 PH0096	Ig heavy chain V r
16	456	73.1	119	2 S31107	Ig heavy chain V r
17	456	73.1	124	2 C27888	Ig heavy chain - h
18	456	73.1	138	2 S31666	Ig heavy chain V r
19	455.5	73.0	112	2 S26327	Ig heavy chain V r
20	454	72.8	117	2 PL0252	Ig heavy chain V r
21	452.5	72.5	121	2 A27888	Ig heavy chain V r
22	452.5	72.5	121	2 S55340	Ig heavy chain V r
23	451.5	72.4	121	2 D27888	Ig heavy chain V r
24	451.5	72.4	121	2 B27888	Ig heavy chain V r
25	450.5	72.2	119	2 D27889	Ig heavy chain V r
26	449.5	72.0	113	2 S26468	Ig heavy chain V r
27	449.5	72.0	121	2 H27887	Ig heavy chain V r
28	448.5	71.9	139	2 S38808	Ig heavy chain - m
29	447.5	71.7	548	2 S38864	Ig epsilon chain

30	447	71.6	152	2 B26471	Ig heavy chain pre
31	446.5	71.6	128	2 S26790	Ig heavy chain V r
32	444.5	71.2	119	2 B27889	Ig heavy chain V r
33	443.5	71.1	121	2 H27888	Ig heavy chain V r
34	443	71.0	119	2 PH0098	Ig heavy chain V r
35	442	70.8	124	2 I27888	Ig heavy chain V r
36	441.5	70.8	108	2 PH1010	Ig heavy chain (su
37	441.5	70.8	118	2 S31105	Ig heavy chain V r
38	441	70.7	119	2 D36005	Ig heavy chain V r
39	440	70.5	125	2 S30531	Ig heavy chain V r
40	439.5	70.4	120	2 S12953	Ig heavy chain V r
41	439.5	70.4	123	2 S63597	Ig heavy chain, v
42	439	70.4	119	2 S31108	Ig heavy chain - h
43	438.5	70.3	123	2 G27888	Ig heavy chain V r
44	438	70.2	140	2 S31686	Ig heavy chain pre
45	437.5	70.1	140	2 S70442	Ig heavy chain pre
46	437	70.0	160	2 S05271	Ig heavy chain pre
47	436.5	70.0	119	2 PH1531	Ig H chain V regio
48	436.5	70.0	122	2 PH1537	Ig H chain V regio
49	435	69.7	123	2 S31114	Ig heavy chain - h
50	434	69.6	123	2 S26794	Ig heavy chain V r
51	434	69.6	213	2 S68213	Ig heavy chain (Ma
52	432.5	69.3	106	2 PH1008	Ig heavy chain V r
53	432.5	69.3	108	2 PL0248	Ig heavy chain V r
54	432.5	69.3	114	2 S31120	Ig heavy chain - h
55	432.5	69.3	120	2 S44111	Ig heavy chain V-D
56	432.5	69.3	124	2 S20782	Ig heavy chain V r
57	431.5	69.2	111	2 PL0199	anti-DNA autoantib
58	431.5	69.2	128	2 S26786	Ig heavy chain V r
59	431.5	69.2	137	2 S78054	Ig heavy chain pre
60	431	69.1	117	1 HVMS34	Ig heavy chain pre
61	430	68.9	119	2 A43413	Ig heavy chain V r
62	429.5	68.8	112	2 A27889	Ig heavy chain V r
63	429.5	68.8	128	2 PH0095	Ig heavy chain V r
64	429.5	68.8	147	2 I37780	Ig kappa chain V r
65	429	68.8	119	2 S36005	Ig variable region
66	429	68.8	135	2 S31598	Ig heavy chain V r
67	429	68.8	139	2 I37781	Ig variable region
68	429	68.8	140	2 S31588	Ig heavy chain V r
69	428.5	68.7	120	2 S48798	Ig heavy chain V r
70	428.5	68.7	139	2 S31674	Ig heavy chain V r
71	428.5	68.5	141	2 S31669	Ig heavy chain V r
72	427.5	68.4	119	2 F36005	Ig heavy chain V r
73	427	68.4	143	2 S23624	Ig heavy chain V r
74	427	68.4	128	2 PH0094	Ig heavy chain V r
75	425.5	68.2	135	2 I37778	Ig variable region
76	425.5	68.1	108	2 PH1006	Ig heavy chain V r
77	425	68.1	142	2 C34903	Ig heavy chain pre
78	424.5	68.0	136	2 S31587	Ig heavy chain V r
79	424.5	68.0	124	2 S20784	Ig heavy chain V r
80	424	67.9	127	2 S38489	Ig heavy chain - h
81	424	67.9	122	2 PH1534	Ig H chain V regio
82	423.5	67.9	122	2 E36005	Ig heavy chain V r
83	423.5	67.9	136	1 GLMS21	Ig heavy chain pre
84	423.5	67.9	121	2 B34871	Ig heavy chain V r
85	423	67.8	121	2 S20772	Ig heavy chain V r
86	422.5	67.7	123	2 S38493	Ig heavy chain - h
87	422	67.6	134	2 S31699	Ig heavy chain V r
88	421.5	67.5	122	2 PC2398	anti-tetanus toxin
89	421.5	67.5	121	2 G36005	Ig heavy chain V r
90	421	67.5	132	2 S31603	Ig heavy chain V r
91	421	67.4	119	2 PH1533	Ig H chain V regio
92	420.5	67.3	134	2 S31679	Ig heavy chain V r
93	420	67.1	111	2 S40090	Ig heavy chain - m
94	419	67.1	117	2 S78486	Ig heavy chain V r
95	419	67.1	121	2 I55673	Ig heavy chain - h
96	419	67.1	121	2 S19666	Ig heavy chain V r
97	419	67.1	110	2 PH1652	Ig heavy chain V r
98	418.5	67.1	114	2 PH1009	Ig heavy chain V r
99	418.5	66.9	128	2 S48797	Ig heavy chain V r
100	417.5				

## ALIGNMENTS

[illegible]

RESULT 2  
S55536  
IG heavy chain V region pe20 - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S55536  
R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
J. Mol. Biol. 247, 332-346, 1995  
A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using mutations in the variable region genes.  
A/Reference number: S55528; MUID:95239763; PMID:7536850  
A/Accession: S55536  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-120 <BOE>  
A/Cross-references: EMBL:X82589; NID:9854304; PIDN:CAA57925.1; PID:9854305  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/14-97/Domain: immunoglobulin homology <IMM>

[illegible]

RESULT 3  
I27887  
Ig heavy chain V region (H37-45) - mouse  
C:Species: Mus musculus (house mouse)  
C:date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C:Accession: I27887

R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986  
A:Title: Structural and functional implications of a restricted antibody response to a de  
A:Reference number: A91043; MUID:86300658; PMID:2427335  
A:Accession: I27887  
A:Molecule type: DNA  
A:Residues: 1-121 <CAT>  
A:Experimental source: strain Balb/c  
A:Note: This sequence was determined from the germline gene  
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus he  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
P:15-98/Domain: immunoglobulin homology <IMM>

	Query Match	75.4%	Score 470.5	DB 2	Length 121	
	Best Local Similarity	76.9%	Pred. No. 8e-37			
	Matches 9	Conservative	8	Mismatches 17	Indels 3	Gaps 1
Qy	1	EVTLVSGGDFVKPGGSLKVC	CAASGAF	SHYAMSVW	QTPAKRLEKVA	ISSGGSGTYY 60
Db	1	EVMLVSGGGLVPGGSLK	CAASGFTF	SIYAMSVW	QTPAKRLEKVA	ISSGGTYY 60
Qy	61	SDSVKGRFTISRDNKNTLY	LOWRS	LRSDDS	AMVFC	TR---VKLGTYYFDQSGQGLTV 117
Db	61	PDVSKGRFTISRDNKNTLY	LOWRS	LRSDDS	TAMVYCAR	BEGGLRLYAMDYWGQTSVTV 120

RESULT 4

IG heavy chain V region pe21 - mouse (fragment)  
S55537  
C:Species: Mus musculus (house mouse)  
C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #tex  
C:Accession: S55537  
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
J. Mol. Biol. 247, 932-946, 1995  
A:Title: Comprehensive epitope analysis of monoclonal a  
utations in the variable region genes.  
A:Reference number: S55528; MUID:95239763; PMID:7536850  
A:Accession: S55537  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-120 <BOE>  
C:Superfamily: EMBL:X85590; NTD:g854306; PIDN:CAAS  
C:Superfamily: immunoglobulin V region; immunoglobulin  
C:Keywords: heterotetramer; immunoglobulin  
F:14-97/Domain: immunoglobulin homology <IMM>

	Query Match	75.2%	Score 469	DB 2	Length 120
	Best Local Similarity	78.3%	Fred. No. 1.1e-36		
	Matches 94	Conservative	5	Mismatches 19	Indels 2
	Gaps 1				
Qy	2	VTLVESGGDFVKPGGSLKVS	CAASGFAFSHYAMSWVRQT	PAKLEWVAYTSSGSGTYY	61
Db	1	VLQESGGGVKPGGSLKLS	CAASRFTFSYAMSWVRQT	PEKLEWVATSSGSGTYY	60
Qy	62	DSVKGRFTISRDNAKNTLY	LQMSLSKESDSAMFCTRV	--KLGTYYFDSVGQGTTLTV	SS 119
Db	61	DSVKGRFTISRDNAKNTLY	LQMSLSKESDAMFYCTRL	YDYDPVYMDYKGGTTLTV	SS 120

RESULT 5  
E27888  
lg heavy chain V region (H35-C6) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C:Accession: E27888  
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986  
A:Title: Structural and functional implications of a restricted antibody re

A;Reference number: A91043; MUID:86300658; PMID:2427335

A;Accession: E27888

A;Molecule type: DNA

A;Residues: 1-122 <CAT>

A;Experimental source: strain Balb/c

A;Note: this sequence was determined from the germline gene

C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus H

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.2%; Score 469; DB 2; Length 122;  
Best Local Similarity 75.4%; Pred. No. 1.1e-35;  
Matches 92; Conservative 8; Mismatches 18; Indels 4; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAPFASHYAMSWVRQTPAKRLEWVAIISGGSGTYY 60

Db 1 DVKLVESGGGLVKPGGSLKLS CAASGFTFSYTMVSRQTPPEKRLEWVAIISGGSGTYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTR----VKLGTYYFDSWGQGTTLT 116

Db 61 PDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRQGEYRYYDDYAMDYWGQGTSTV 120

QY 117 VS 118

Db 121 VS 122

#### RESULT 6

PH1007

IG heavy chain V region (clone 163-cl) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PH1007

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH1007

A;Molecule type: mRNA

A;Residues: 1-111 <TL>

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.8%; Score 467; DB 2; Length 111;  
Best Local Similarity 82.0%; Pred. No. 1.5e-36;  
Matches 91; Conservative 3; Mismatches 15; Indels 2; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAPFASHYAMSWVRQTPAKRLEWVAIISGGSGTYY 60

Db 1 EVKLVESGGGLVKPGGSLKLS CAASGFTFSYAMSWVRQTPAKRLEWVAIISGGSGTYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVLG--TYFDSW 109

Db 61 PDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYCASHYYSRTYYFDYW 111

#### RESULT 7

F27888

IG heavy chain V region (H158-89H4) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996

C;Accession: F27888

R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A;Title: Structural and functional implications of a restricted antibody response to a c

A;Reference number: A91043; MUID:86300658; PMID:2427335

A;Accession: F27888

A;Molecule type: DNA

A;Residues: 1-119 <CAT>

A;Experimental source: strain Balb/c

A;Note: this sequence was determined from the germline gene

C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus he

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.8%; Score 466.5; DB 2; Length 119;  
Best Local Similarity 76.9%; Pred. No. 1.8e-36;  
Matches 93; Conservative 8; Mismatches 15; Indels 5; Gaps 2;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAPFASHYAMSWVRQTPAKRLEWVAIISGGSGTYY 60

Db 1 DVKLVESGGGLVKPGGSLKLS CAASGFTFSYTMVSRQTPPEKRLEWVAIISGGSGTYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVLKGTYY---PDSWGQGTTLTV 117

Db 61 PDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCRGE--TYDYAMDYWGQGTSTVV 118

QY 118 S 118

Db 119 S 119

#### RESULT 8

S09258

IG heavy chain V region precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 23-Jul-1999

C;Accession: S09258

R;Hamada, H.; Maezawa, K.; Tsuruo, T.

Nucleic Acids Res. 18, 1900, 1990

A;Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRX1

A;Reference number: S09258; MUID:90245594; PMID:2110659

A;Accession: S09258

A;Molecule type: DNA

A;Residues: 1-138 <HAM>

A;Cross-references: EMBL:X51719; NID:G53207; PIDN:CAA36012.1; PID:G297545

C;Genetics:

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 464; DB 2; Length 138;  
Best Local Similarity 75.6%; Pred. No. 3.7e-36;  
Matches 90; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAPFASHYAMSWVRQTPAKRLEWVAIISGGSGTYY 60

Db 20 EVILVESGGGLVKPGGSLKLS CAASGFTFSYTMVSRQTPPEKRLEWVAIISGGGNTYY 79

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVLKGTYYPDSWGQGTTLTVSS 119

Db 80 PDSVKGRFTISRDNKNTLYLQMSLRSEDSALYCYARYRYEAFASWGQGTTLTVSA 138

#### RESULT 9

S55539

IG heavy chain V region pe24 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999

C;Accession: S55539

R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using

utations in the variable region genes.

A;Reference number: S55528; MUID:95239763; PMID:7536850

A;Accession: S55539

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-120 <BOE>

A;Cross-references: EMBL:X82593; NID:G854312; PIDN:CAA57929.1; PID:G854313

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 463; DB 2; Length 120;  
Best Local Similarity 76.7%; Pred. No. 3.9e-36;  
Matches 92; Conservative 6; Mismatches 20; Indels 2; Gaps 1;

QY 2 VTLLVESGGDFVKPGGSLKVS CAASGFAPSHYAMSWVRQTPAKRLWVAYISSGGSGTYYS 61  
DB 1 VQLQSSGGGLVKPGGSLKLS CAASGFTFSYAMSWVRQTPKRLWVATISSGGSGTYYP 60  
QY 62 DSVKGRFTISRDNKNTLYLQMSRLSRSDSAMVFCFTRV--KLGTYYFDSWGQTTTLTVSS 119  
DB 61 DSVKGRFTISRDNKNTLYLQMSRLSRSDTAMYYCRLYYDYDPYMDYWGQTTTLTVSS 120

## RESULT 10

PH0097  
Ig heavy chain V region (anti-cyclosporin B) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 16-Aug-1996  
C:Accession: PH0097  
R:Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Koher, H.P.; Quesniaux, V.F.J.; V  
Mol. Immunol. 27, 1029-1038, 1990  
A:Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.  
A:Reference number: PH0087; MUID:91042849; PMID:2122240  
A:Accession: PH0097  
A:Molecule type: mRNA  
A:Residues: 1-118 <SCH>

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:50-66/Region: complementarity-determining 2  
F:99-105/Region: complementarity-determining 3

Query Match 74.1%; Score 462.5; DB 2; Length 118;  
Best Local Similarity 79.0%; Pred. No. 4.3e-36;  
Matches 94; Conservative 4; Mismatches 18; Indels 3; Gaps 1;

QY 1 EYTLVESGGDFVKPGGSLKVS CAASGFAPSHYAMSWVRQTPAKRLWVAYISSGGSGTYYS 60  
DB 1 DVKLVESGGGLVKPGGSLKLS CAASGFTFSYIMSWVRQTPKRLWVATISSGGRYYY 60  
QY 61 SDSVKGRFTISRDNKNTLYLQMSRLSRSDSAMVFCFTRVKLTYYFDSWGQTTTLTVSS 119  
DB 61 SDSVKGRFTISRDNKNTLYLQMSRLSRSDTAMYYTST---ASGDSFDYWGQTTTLTVSS 116

## RESULT 11

S20641  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S20641  
R:Lozman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.  
submitted to the EMBL Data Library, February 1992  
A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice react  
A:Reference number: S20639  
A:Accession: S20641  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-118 <LOS>

C:Cross-references: EMBL:X65003; NID:G52602; PIDN:CAA46136.1; PID:G52603  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 462; DB 2; Length 118;  
Best Local Similarity 75.4%; Pred. No. 4.8e-36;  
Matches 89; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

QY 1 EYTLVESGGDFVKPGGSLKVS CAASGFAPSHYAMSWVRQTPAKRLWVAYISSGGSGTYYS 60  
DB 1 EVKLVESGGGLVKPGGSLKLS CAASGFTFSYIMFWVRQTPAKRLWVATISSGGSGTYYP 60  
QY 61 SDSVKGRFTISRDNKNTLYLQMSRLSRSDSAMVFCFTRVKLTYYFDSWGQTTTLTVSS 118  
DB 61 PDSVKGRFTISRDNKNTLYLQMSRLSRSDTAMYYCARRAYSNYALDFWQGTSTVTS 118

## RESULT 12

PL0249  
Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
C:Accession: PL0249  
R:Shiomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rochstein, A.  
J. Exp. Med. 171, 265-297, 1990  
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n  
A:Reference number: PL0231; MUID:90111618; PMID:2104919  
A:Accession: PL0249  
A:Molecule type: mRNA  
A:Residues: 1-117 <SHU>

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-30/Region: framework 1  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:36-49/Region: framework 2  
F:50-66/Region: complementarity-determining 2  
F:67-98/Region: framework 3  
F:99-108/Region: complementarity-determining 3  
F:109-117/Region: framework 4

Query Match 73.9%; Score 461; DB 2; Length 117;  
Best Local Similarity 75.2%; Pred. No. 5.9e-36;  
Matches 88; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 1 EYTLVESGGDFVKPGGSLKVS CAASGFAPSHYAMSWVRQTPAKRLWVAYISSGGSGTYYS 60  
DB 1 EVKLVESGGGLVKPGGSLKLS CAASGFTFSYIMSWVRQTPAKRLWVATISSGGSGTYYP 60  
QY 61 SDSVKGRFTISRDNKNTLYLQMSRLSRSDSAMVFCFTRVKLTYYFDSWGQTTTLTV 117  
DB 61 PDSVKGRFTISRDNKNTLYLQMSRLSRSDTAMYYCARRDYSHWFFDVWGATTTVT 117

## RESULT 13

S55538  
Ig heavy chain V region pe22 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S55538  
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
J. Mol. Biol. 247, 932-946, 1995  
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using  
utations in the variable region genes  
A:Reference number: S55528; MUID:95239763; PMID:7536850  
A:Accession: S55538  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-120 <BOE>

C:Cross-references: EMBL:X82591; NID:G854308; PIDN:CAA57927.1; PID:G854309  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 73.7%; Score 460; DB 2; Length 120;  
Best Local Similarity 75.8%; Pred. No. 7.5e-36;  
Matches 91; Conservative 7; Mismatches 20; Indels 2; Gaps 1;

QY 2 VTLLVESGGDFVKPGGSLKVS CAASGFAPSHYAMSWVRQTPAKRLWVAYISSGGSGTYYS 61  
DB 1 VKLQSSGGGLVKPGGSLKLS CAASGFTFSYAMSWVRQTPKRLWVATISSGGNYTYP 60



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:55 ; Search time 30.8793 Seconds  
(without alignments)  
1973.408 Million cell updates/sec

Title: US-10-089-500-55

Perfect score: 624

Sequence: 1 EVTLVSGGDFVKPGSLKV.....KLGTYYFDSNGQGTTLTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	469	75.2	255	2	Q6KB05 mus musculus
2	468.5	75.1	487	2	Q99KA4 mus musculus
3	463	74.2	119	2	Q920E7 mus musculus
4	455	72.9	486	2	Q91207 mus musculus
5	450	72.1	479	2	Q91WP5 mus musculus
6	439.5	70.4	473	2	Q91205 mus musculus
7	431.5	69.2	606	2	Q6GMY2 mus musculus
8	431	69.1	117	1	Q9UL71 mus musculus
9	430	68.9	121	2	Q9UL71 mus musculus
10	429	68.8	480	2	Q65ZL8 mus musculus
11	426	68.3	196	2	Q65ZL8 mus musculus
12	426	68.3	478	2	Q6PI81 mus musculus
13	425	68.1	464	2	Q6MZU6 mus musculus
14	424	67.9	485	2	Q6PDB8 mus musculus
15	423.5	67.9	136	1	HV16_MOUSE
16	419.5	67.2	465	2	Q6P6C4 mus musculus
17	417	66.8	117	1	HV54_MOUSE
18	417	66.8	470	2	Q6PJA4 mus musculus
19	414.5	66.4	97	1	HV56_MOUSE
20	414.5	66.4	118	2	Q9UL91 mus musculus
21	413	66.2	248	2	Q65ZQ7 mus musculus
22	413	66.2	493	2	Q6GMX2 mus musculus
23	412.5	66.1	613	2	Q8WUK1 mus musculus
24	410	65.7	113	2	Q9UL90 mus musculus
25	410	65.7	597	2	Q96BB9 mus musculus
26	407.5	65.3	118	2	Q9UL72 mus musculus
27	407.5	65.3	494	2	Q96K68 mus musculus
28	407	65.2	98	1	HV57_MOUSE
29	406	65.1	117	1	HV57_MOUSE
30	406	65.1	240	2	Q65ZC9 mus musculus
31	405	64.9	116	2	Q9UL93 mus musculus

32	404.5	64.8	473	2	Q6MZV7	Q6mzv7 homo sapien
33	403.5	64.7	475	2	Q6MZQ6	Q6mzg6 homo sapien
34	401.5	64.3	122	1	HV3Q_HUMAN	P01768 homo sapien
35	400.5	64.2	573	2	Q8WUJ8	Q8wuj8 homo sapien
36	399.5	64.0	471	2	Q66K04	Q66k04 mus musculus
37	398	63.8	499	2	Q8NSK4	Q8nsk4 homo sapien
38	397.5	63.7	112	2	Q9HCC1	Q9hcc1 homo sapien
39	396	63.5	472	2	Q6N089	Q6n089 homo sapien
40	395.5	63.4	147	2	Q9Y509	Q9y509 homo sapien
41	393.5	63.1	122	2	Q9UL84	Q9ul84 homo sapien
42	391.5	62.7	119	1	HV38_MOUSE	P01808 mus musculus
43	391.5	62.7	479	2	Q6MZV6	Q6mzv6 homo sapien
44	391	62.7	121	1	HV3J_HUMAN	P01771 homo sapien
45	390.5	62.6	475	2	Q6GMW7	Q6gmw7 homo sapien
46	390	62.5	117	1	HV59_MOUSE	P18530 mus musculus
47	390	62.5	493	2	Q8NCI6	Q8nci6 homo sapien
48	389.5	62.4	484	2	Q8VEA0	Q8vea0 mus musculus
49	389	62.3	487	2	Q80Z17	Q80z17 mus musculus
50	387.5	62.1	122	1	HV3A_HUMAN	P01762 homo sapien
51	387.5	62.1	487	2	Q6ZVX0	Q6zvx0 homo sapien
52	385	61.7	117	1	HV02_CANFA	P01785 canis fami
53	385	61.7	117	1	HV3C_HUMAN	P01764 homo sapien
54	383.5	61.5	116	1	HV3T_HUMAN	P01781 homo sapien
55	383	61.4	119	1	HV3I_HUMAN	P01770 homo sapien
56	383	61.4	480	2	Q6N094	Q6n094 homo sapien
57	382	61.2	115	1	HV3D_HUMAN	P01763 homo sapien
58	382	61.2	118	1	HV39_MOUSE	P01809 mus musculus
59	381	61.1	466	2	Q6IN78	Q6in78 homo sapien
60	380.5	61.0	126	1	HV3K_HUMAN	P01772 homo sapien
61	380	60.9	117	1	HV53_MOUSE	P18534 mus musculus
62	378.5	60.7	114	1	HV3B_HUMAN	P01763 homo sapien
63	378.5	60.7	544	2	Q6PJ95	Q6pj95 homo sapien
64	377.5	60.5	483	2	Q6MZX9	Q6mzx9 homo sapien
65	376.5	60.3	122	1	HV20_MOUSE	P01789 mus musculus
66	375	60.1	115	1	HV3F_HUMAN	P01767 homo sapien
67	374.5	60.0	114	1	HV01_CANFA	P01784 canis fami
68	371.5	59.5	122	1	HV3H_HUMAN	P01769 homo sapien
69	370.5	59.4	111	1	HV35_MOUSE	P01804 mus musculus
70	370.5	59.4	494	2	Q6ZM64	Q6zm64 homo sapien
71	370	59.3	119	1	HV3L_HUMAN	P01773 homo sapien
72	370	59.3	120	1	HV3E_HUMAN	P01766 homo sapien
73	367.5	58.9	122	1	HV21_MOUSE	P01790 mus musculus
74	367	58.8	123	1	HV18_MOUSE	P01787 mus musculus
75	366.5	58.7	116	1	HV05_CARAU	P19181 carassius a
76	366.5	58.7	120	1	HV3U_HUMAN	P01782 homo sapien
77	366.5	58.7	298	2	Q9QYF0	Q9qyf0 synthetic c
78	366	58.7	466	2	Q6N096	Q6n096 homo sapien
79	365	58.5	123	1	HV19_MOUSE	P01788 mus musculus
80	364.5	58.4	119	1	HV37_MOUSE	P01807 mus musculus
81	364.5	58.4	123	1	HV23_MOUSE	P01792 mus musculus
82	363	58.2	117	1	HV41_MOUSE	P01811 mus musculus
83	363	58.2	144	1	HV26_MOUSE	P01795 mus musculus
84	362.5	58.1	614	2	Q6DDQ7	Q6ddq7 xenopus lae
85	362	58.0	464	2	Q6PIP8	Q6pip8 mus musculus
86	361.5	57.9	473	2	Q6P055	Q6p055 homo sapien
87	361	57.9	123	1	HV24_MOUSE	P01793 mus musculus
88	360	57.7	123	1	HV25_MOUSE	P01794 mus musculus
89	359	57.5	95	2	Q9UL86	Q9ul86 homo sapien
90	359	57.5	123	1	HV22_MOUSE	P01791 mus musculus
91	358.5	57.5	119	1	HV3N_HUMAN	P01775 homo sapien
92	358	57.4	115	1	HV32_MOUSE	P01801 mus musculus
93	358	57.4	519	2	HV30_MOUSE	Q6n092 homo sapien
94	357.5	57.3	119	1	HV3M_HUMAN	P01774 homo sapien
95	357	57.2	131	2	Q9UL88	Q9ul88 homo sapien
96	357	57.2	470	2	Q725W1	Q725w1 homo sapien
97	355	56.9	458	2	Q65ZQ1	Q65zq1 homo sapien
98	355	56.9	593	2	Q6INM5	Q6inm5 xenopus lae
99	354.5	56.8	119	1	HV40_MOUSE	P01810 mus musculus
100	353	56.6	117	1	HV42_MOUSE	P01812 mus musculus

ALIGNMENTS

```
RESULT 1
Q6KB05 PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SCFV BBE5 protein (Fragment).
DE Name=SCFV BBE5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ746180; CAG34081.1; -.
DR HSSP; P01837; 1KCR.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON TER 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 75.2%; Score 469; DB 2; Length 255;
Best Local Similarity 77.0%; Pred. No. 1.2e-40;
Matches 94; Conservative 7; Mismatches 17; Indels 4; Gaps 2;

QY 1 EVTLVESGGDFVKPGSLKVSAAAGFAFHYAMSWVRQTPAKRLWVAYISSGGSGTY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 QVQLQSGDGLVKPGSLKVSAAAGFTFSYGMVSRVQTPDKRLWVATITSGSGYTY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMFYCTRVKLTGY---FDSWGQQTTLTV 117
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 PDSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYICAR-HINRYDGAFDYWGQQTTLTV 119

QY 118 SS 119
Db |||
120 SS 121

RESULT 2
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stachleon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RA Director MGC Project;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004786; AAH04786.1; -.
DR HSSP; P01810; 2PEJ.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 75.1%; Score 468.5; DB 2; Length 487;
Best Local Similarity 75.0%; Pred. No. 2.7e-40;
Matches 93; Conservative 7; Mismatches 19; Indels 5; Gaps 1;

QY 1 EVTLVESGGDFVKPGSLKVSAAAGFAFHYAMSWVRQTPAKRLWVAYISSGGSGTY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 EVQLVESGGDLVKPGSLKLSAAAGFTFSYGMVSRVQTPDKRLWVATITSGSGYTY 79

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMFYCTRVKLTGY----FDSWGQQTTL 115
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 PDSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYICARDMGSPYGGYSRFDYWGQGTI 139

QY 116 TVSS 119
Db ||||
140 TVSS 143

RESULT 3
Q920E7 PRELIMINARY; PRT; 119 AA.
AC Q920E7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307937; AAL09421.1; -.
DR PIR; C25913; C25913.
DR HSSP; P01783; 1IGC.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 119
SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;
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Query Match		74.2%; Score 463; DB 2; Length 119;
Best Local Similarity		77.9%; Pred. No. 2.1e-40;
Matches		94; Conservative 6; Mismatches 17; Indels 4; Gaps 2;
QY	1	EVTLVESGGDFVKPGSLKVCASGAFASHYAMSWVROTPAKRLEWVAIISGGSGTTY 60
DB	1	EVQLVESGGDLVPPGSLKLSKASGFTFSYGMVSWVROTPDKRLEWVAIISGGSGTTY 60
QY	61	SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 118
DB	61	PDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTY--HGDDYDVGFAWGGQTLTVS 118
QY	119 S	119
DB	119 A	119
RESULT 4		
ID	Q91207	PRELIMINARY; PRT; 486 AA.
AC	Q91207	
DT	01-DEC-2001	(TrEMBLrel. 19, Created)
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)
DE	Igh-VJ558 protein.	
GN	Names=Igh-VJ558;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=CZECH II; TISSUE=Mammary tumor;	
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klauser R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,	
RA	Jones S.J., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=CZECH II; TISSUE=Mammary tumor;	
RA	Director MGC Project;	
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC010324; AAH0324.1; -	
DR	HSSP; P01789; IMCP.	
DR	Pfam; PF07654; Cl-set; 2.	
DR	SMART; SM00406; IGV; 1.	
DR	PROSITE; PS00835; IG LIKE; 4.	
DR	PROSITE; PS00290; IG_MHC; UNKNOWN 2.	
SQ	SEQUENCE 486 AA; 52681 MW; 4FEF83125DA0870B CRC64;	
Query Match		72.9%; Score 455; DB 2; Length 486;
Best Local Similarity		71.0%; Pred. No. 6.9e-39;
Matches		88; Conservative 14; Mismatches 16; Indels 6; Gaps 2;
QY	1	EVTLVESGGDFVKPGSLKVCASGAFASHYAMSWVROTPAKRLEWVAIISGGSGTTY 60
DB	1	EVQLVESGGDLVPPGSLKLSKASGFTFSYGMVSWVROTPDKRLEWVAIISGGSGTTY 60
QY	61	SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 118
DB	61	PDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTY--HGDDYDVGFAWGGQTLTVS 118
QY	119 S	119
DB	119 A	119
RESULT 5		
ID	Q91WP5	PRELIMINARY; PRT; 479 AA.
AC	Q91WP5	
DT	01-DEC-2001	(TrEMBLrel. 19, Created)
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)
DE	Igh-VJ558 protein.	
GN	Mus musculus (Mouse).	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=FVB/N; TISSUE=Colon;	
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klauser R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,	
RA	Jones S.J., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=FVB/N; TISSUE=Colon;	
RA	Strausberg R.;	
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC013656; AAH13656.1; -	
DR	HSSP; P01789; IMCP.	
DR	Pfam; PF07654; Cl-set; 2.	
DR	SMART; SM00406; IGV; 1.	
DR	PROSITE; PS00835; IG LIKE; 4.	
DR	PROSITE; PS00290; IG_MHC; UNKNOWN 2.	
SQ	SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;	
Query Match		72.1%; Score 450; DB 2; Length 479;
Best Local Similarity		73.9%; Pred. No. 2.2e-38;
Matches		88; Conservative 9; Mismatches 18; Indels 4; Gaps 1;
QY	1	EVTLVESGGDFVKPGSLKVCASGAFASHYAMSWVROTPAKRLEWVAIISGGSGTTY 60
DB	20	EVQLVESGGGLVPPGSLKLSKASGFTFSYGMVSWVROTPDKRLEWVAIISGGSGTTY 79
QY	61	SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 119
DB	80	SUTMKGRTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTY--GGYFDVWGAGTAVTVSS 134

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RESULT 6
Q91Z05 PRELIMINARY; PRT; 473 AA.
ID Q91Z05;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Expressed sequence AU044919.
GN Name=AU044919;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAINS=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
SEQUENCE FROM N.A.
RC STRAINS=CZECH II; TISSUE=Mammary tumor;
RX STRAIN=Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -.
DR F1; S68213; S68213.
DR HSP; P01783; I1GC.
DR MGD; MGI:2144967; AU044919.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 70.4%; Score 439.5; DB 2; Length 473;
Best Local Similarity 72.3%; Pred. No. 2.8e-37; Indels 1; Gaps 1;
Matches 86; Conservative 10; Mismatches 22;

QY 1 EYTLVESGGDFVKPGSLKVS CAASGFAFSHYAMSWVRQTPAKRLWEVAYISGGSGTYY 60
DB 20 EVQLVESGGGLVKPGSRKLS CAASGFTFSDYGMHWVRQAPKGLWEVAYISGGSTIYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLGTYTFDSWGQQTTLTVSS 119
DB 80 ADTVKGRFTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLGTYTFDSWGQQTTLTVSS 137

RESULT 7
Q6GMY2 PRELIMINARY; PRT; 606 AA.
ID Q6GMY2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Expressed sequence AU044919.
GN Name=AU044919;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAINS=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
SEQUENCE FROM N.A.
RC STRAINS=CZECH II; TISSUE=Mammary tumor;
RX STRAIN=Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -.
DR F1; S68213; S68213.
DR HSP; P01783; I1GC.
DR MGD; MGI:2144967; AU044919.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 70.4%; Score 439.5; DB 2; Length 473;
Best Local Similarity 72.3%; Pred. No. 2.8e-37; Indels 1; Gaps 1;
Matches 86; Conservative 10; Mismatches 22;

QY 1 EYTLVESGGDFVKPGSLKVS CAASGFAFSHYAMSWVRQTPAKRLWEVAYISGGSGTYY 60
DB 20 EVQLVESGGGLVKPGSRKLS CAASGFTFSDYGMHWVRQAPKGLWEVAYISGGSTIYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLGTYTFDSWGQQTTLTVSS 119
DB 80 ADTVKGRFTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLGTYTFDSWGQQTTLTVSS 137

RESULT 8
HV55_MOUSE PRELIMINARY; PRT; 117 AA.
ID HV55_MOUSE;
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE Expressed sequence AU044919.
GN Name=AU044919;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAINS=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
SEQUENCE FROM N.A.
RC STRAINS=CZECH II; TISSUE=Mammary tumor;
RX STRAIN=Strausberg R.;
RL Submitted (JUN-2004); AAH73758.1; -.
DR EMBL; BC073758; AAH73758.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 606 AA; 66184 MW; B6B38B51114B4C55 CRC64;

Query Match 69.2%; Score 431.5; DB 2; Length 606;
Best Local Similarity 64.2%; Pred. No. 2.5e-36;
Matches 86; Conservative 13; Mismatches 20; Indels 15; Gaps 2;

QY 1 EYTLVESGGDFVKPGSLKVS CAASGFAFSHYAMSWVRQTPAKRLWEVAYISGGSGTYY 60
DB 20 EVQLVESGGGLVKPGSRKLS CAASGFTFSDYGMHWVRQAPKGLWEVAYISGGSTIYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLGTYTFDSWGQQTTLTVSS 106
DB 80 ADTVKGRFTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLGTYTFDSWGQQTTLTVSS 139
QY 107 -DSWGQQTTLTVSS 119
DB 140 MDVWGQQTTLTVSS 153

RESULT 9
HV55_MOUSE PRELIMINARY; PRT; 117 AA.
ID HV55_MOUSE;
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE Expressed sequence AU044919.
GN Name=AU044919;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAINS=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
SEQUENCE FROM N.A.
RC STRAINS=CZECH II; TISSUE=Mammary tumor;
RX STRAIN=Strausberg R.;
RL Submitted (JUN-2004); AAH73758.1; -.
DR EMBL; BC073758; AAH73758.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 606 AA; 66184 MW; B6B38B51114B4C55 CRC64;

Query Match 69.2%; Score 431.5; DB 2; Length 606;
Best Local Similarity 64.2%; Pred. No. 2.5e-36;
Matches 86; Conservative 13; Mismatches 20; Indels 15; Gaps 2;

QY 1 EYTLVESGGDFVKPGSLKVS CAASGFAFSHYAMSWVRQTPAKRLWEVAYISGGSGTYY 60
DB 20 EVQLVESGGGLVKPGSRKLS CAASGFTFSDYGMHWVRQAPKGLWEVAYISGGSTIYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLGTYTFDSWGQQTTLTVSS 106
DB 80 ADTVKGRFTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKLGTYTFDSWGQQTTLTVSS 139
QY 107 -DSWGQQTTLTVSS 119
DB 140 MDVWGQQTTLTVSS 153
```



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Query Match      68.8%; Score 429; DB 2; Length 480;
Best Local Similarity 70.8%; Pred. No. 3.5e-36;
Matches 85; Conservative 13; Mismatches 18; Indels 4; Gaps 2;

QY 1 EVTLVESGGDFVKPGGSLKVS CAAGFAFASHYAMSWVRQTTPAKRLIEWAYISSGGSGTY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 19 DVKLVESGGGLVKPGGSLKVS CAAGFAFASHYAMSWVRQTTPAKRLIEWATISNGVATHY 78
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTY-YFDSWGGGTTTLTVSS 119
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 79 PDSMKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTY-YFDSWGGGTTTLTVSS 135
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
Q55ZL8 PRELIMINARY; PRT; 196 AA.
AC Q65ZL8;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE VH7183-DSP2-JH3-CHI protein (Fragment)
GN Name=VH7183-DSP2-JH3-CHI;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=95362300; PubMed=7635518;
RA Komori T., Sugiyama H.;
RT "An aberrant splicing using a 3' cryptic splice site within the CHI
RL exon induces truncated mu-chain production."
RL Immunology 85:166-170(1995).
DR EMBL; S79401; AAB35023.2; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 196
SQ SEQUENCE 196 AA; 21429 MW; 12A381018944B268 CRC64;

Query Match      68.3%; Score 426; DB 2; Length 196;
Best Local Similarity 86.5%; Pred. No. 2.7e-36;
Matches 83; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVKPGGSLKVS CAAGFAFASHYAMSWVRQTTPAKRLIEWAYISSGGSGTY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EYMLVESGGGLVKPGGSLKVS CAAGFTFSSYAMSWVRQTTPAKRLIEWATISNGSYTY 79
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFC 96
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 PDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFC 115
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
Q5PI81 PRELIMINARY; PRT; 478 AA.
AC Q6PI81;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC041037; AAH41037.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match      68.3%; Score 426; DB 2; Length 478;
Best Local Similarity 66.7%; Pred. No. 7.1e-36;
Matches 86; Conservative 10; Mismatches 23; Indels 10; Gaps 2;

QY 1 EVTLVESGGDFVKPGGSLKVS CAAGFAFASHYAMSWVRQTTPAKRLIEWAYISSGGSGTY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVQLVESGGGLVQPGGSLRLS CAASGFTFSSYAMSWVRQAPGKLEWVANIKQDGEKYY 79
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTR-----VKLGTYF--DSWG 110
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 VDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTR-----VKLGTYF--DSWG 139
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 111 QGTTTLTVSS 119
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 140 KGTIVTVSS 148
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
Q6MZU6 PRELIMINARY; PRT; 464 AA.
AC Q6MZU6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C15213.
GN Name=DKFZp686C15213;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

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RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloembergen R.;
RG The German Human cDNA Consortium;
RA Bloembergen R., Boecher M., Newes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CA245931.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003596; Ig v.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;

Query Match 68.1%; Score 425; DB 2; Length 464;
Best Local Similarity 70.0%; Pred. No. 8.8e-36;
Matches 84; Conservative 14; Mismatches 20; Indels 2; Gaps 2;

QY 1 EVTLVSGGDFVKPGGSLKVSAAAGFAFASHYAMSVWROTPAKRLWVAVYISS-GGSGTY 59
DB 20 EVTLVSGGDFVKPGGSLKVSAAAGFAFASHYAMSVWROTPAKRLWVAVYISS-GGSGTY 59
QY 60 YDSVKGRTISRDNKNTLYLQMSRLSRSDSAMYFCTRVKLTGY--YFDSWGQGTTLTVSS 119
DB 80 YDSVKGRTISRDNKNTLYLQMSRLSRSDSAMYFCTRVKLTGY--YFDSWGQGTTLTVSS 119

RESULT 14
Q6PDB8 PRELIMINARY; PRT; 485 AA.
AC Q6PDB8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S.C., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smallos D.E., Schnarch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
```

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RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059814; AAH59814.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 485 AA; 52472 MW; 81236FF3AD821056 CRC64;

Query Match 67.9%; Score 424; DB 2; Length 485;
Best Local Similarity 67.8%; Pred. No. 1.2e-35;
Matches 82; Conservative 12; Mismatches 25; Indels 2; Gaps 1;

QY 1 EVTLVSGGDFVKPGGSLKVSAAAGFAFASHYAMSVWROTPAKRLWVAVYISSGGSGTY 60
DB 20 EVTLVSGGDFVKPGGSLKVSAAAGFAFASHYAMSVWROTPAKRLWVAVYISSGGSGTY 60
QY 61 SDSVKGRTISRDNKNTLYLQMSRLSRSDSAMYFCTRVKLTGY--YFDSWGQGTTLTVSS 118
DB 80 ADSVKGRTISRDNKNTLYLQMSRLSRSDSAMYFCTRVKLTGY--YFDSWGQGTTLTVSS 118
QY 119 S 119
DB 140 S 140

RESULT 15
HV16 MOUSE STANDARD; PRT; 136 AA.
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adetugbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
CC -----
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CC -----
DR EMBL; J00522; AAD15290.1; -.
DR PIR; E90809; G1MS21.
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DR	PDB; 1IGC; X-ray; H=.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF00047; ig; 1.		
DR	SMART; SM00406; IgV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
KW	3D-structure; Direct protein sequencing; Immunoglobulin V region;		
KW	Signal.		
FT	NON TER	1	
FT	FT	1	
FT	SIGNAL	<1	16
FT	CHAIN	17	136
FT	DOMAIN	115	119
FT	DOMAIN	120	136
FT	DISULFID	38	112
FT	CONFLICT	75	78
FT	CONFLICT	89	90
FT	CONFLICT	115	115
FT	CONFLICT	120	120
FT	STRAND	19	23
FT	STRAND	26	28
FT	TURN	30	31
FT	STRAND	34	41
FT	HELIX	45	47
FT	STRAND	50	55
FT	STRAND	61	67
FT	TURN	69	70
FT	STRAND	74	76
FT	HELIX	78	80
FT	STRAND	81	81
FT	TURN	82	83
FT	STRAND	84	89
FT	TURN	90	93
FT	STRAND	94	99
FT	HELIX	104	106
FT	STRAND	108	114
FT	TURN	118	119
FT	STRAND	125	126
FT	STRAND	130	134
FT	NON TER	136	136
SO	SEQUENCE	136 AA;	15071 MW; 2276A98BDB3F7016 CRC64;



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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:10 ; Search time 32.5277 Seconds  
(without alignments)  
1284.140 Million cell updates/sec

Title: US-10-089-500-56  
Perfect score: 572  
Sequence: 1 DIQMTQASSLPASLGDRVT.....HQYSKLPWTFGGTKLEIKR 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	572	100.0	108	4	AAB81990
2	572	100.0	108	6	ABU11013
3	572	100.0	128	3	AAB01628
4	572	100.0	128	4	AAB81978
5	572	100.0	128	6	ABU11003
6	564	98.6	128	2	AAZ28368
7	562	98.3	128	2	AAR33257
8	557	97.4	128	2	AAR33340
9	521	91.1	108	2	AAW00834
10	520	90.9	127	2	AAR12359
11	516	90.2	108	2	AAW04177
12	516	90.2	108	2	AAW16620
13	516	90.2	128	4	AAB81998
14	516	90.2	650	6	ABR62591
15	516	90.2	651	6	ABR62590
16	515	90.0	126	2	AAR12237
17	514	89.9	108	4	AAB81988
18	514	89.9	128	4	AAB81999
19	511	89.3	128	4	AAB81992
20	510	89.2	108	2	AAW70620
21	510	89.2	108	5	ABP61189
22	508	88.8	108	6	ABU11011
23	507	88.6	128	4	AAB81994
24	507	88.6	214	8	ADN41870
25	506	88.5	128	4	AAB81995

99 474 82.9 667 6 ABP97414 Anti-huma  
100 473 82.7 127 2 AAR29010 p146-k3 p

## ALIGNMENTS

## RESULT 1

AAB81990 AAB81990 standard; protein; 108 AA.

XX AC AAB81990;  
XX DT 03-JUL-2001 (first entry)  
XX DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 56.  
XX KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
XX KW cancer.  
XX OS Mus musculus.  
XX PN WO200123432-A1.  
XX PD 05-APR-2001.  
XX PF 29-SEP-2000; 2000WO-JP006774.  
XX PR 30-SEP-1999; 99JP-00278291.  
XX PR 06-APR-2000; 2000JP-00105088.  
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX WPI; 2001-266143/27.

XX DT New human type complementation-determining region-transplanted antibody,  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.

XX Claim 11; Page 174-175; 183pp; Japanese.

XX CC The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumors, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 572; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.4e-39;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 60  
DB 1 DIQMTQTASSLPASLGDRVTISCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 60  
QY 61 RPSGGSGGTDYSLTISNLEPEDATYFCHQYSKLPWTFGGGKLEIKR 108  
DB 61 RPSGGSGGTDYSLTISNLEPEDATYFCHQYSKLPWTFGGGKLEIKR 108

## RESULT 2

ABU11013 ABU11013 standard; protein; 108 AA.

XX AC ABU11013;  
XX DT 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #6.  
XX KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.  
XX OS Mus musculus.  
XX PN WO200278739-A1.  
XX PD 10-OCT-2002.  
XX PF 29-MAR-2002; 2002WO-JP003170.  
XX PR 29-MAR-2001; 2001JP-00097483.  
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX PI Shitara K, Niwa R, Kanazawa J, Asada M;  
XX WPI; 2003-067410/06.  
XX PS Claim 7; Page 113; 121pp; Japanese.

XX CC The invention describes drugs contain a genetically-modified antibody  
CC against ganglioside GD3 or its fragment and at least 1 of a substance  
CC capable of activating immunocompetent cells and a substance having an  
CC antitumor activity in combination. The drugs can be used to treat tumour  
CC like melanoma and can provide a treatment with enhanced therapeutic  
CC effect and little side-reactions, particularly to relieve problems of  
CC side-effects during the conventional single administration. This sequence  
CC represents a protein associated with the anti- ganglioside GD3 antibody

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 572; DB 6; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.4e-39;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 60  
DB 1 DIQMTQTASSLPASLGDRVTISCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 60  
QY 61 RPSGGSGGTDYSLTISNLEPEDATYFCHQYSKLPWTFGGGKLEIKR 108  
DB 61 RPSGGSGGTDYSLTISNLEPEDATYFCHQYSKLPWTFGGGKLEIKR 108

## RESULT 3

AAB01628 AAB01628 standard; protein; 128 AA.

XX AC AAB01628;  
XX DT 07-DEC-2000 (first entry)  
XX DE Murine immunoglobulin light chain variable region.

XX KW Mouse; immunoglobulin; L chain; light chain; variable region; cancer;  
XX KW humanised antibody.

XX OS Mus sp.

XX FH Key Location/Qualifiers  
XX FT Peptide 1..20  
XX FT /label= signal\_peptide  
XX FT Protein 21..128  
XX FT /label= mature\_immunoglobulin\_light\_chain\_v\_region

XX PN EP1013761-A2.

```

PD 28-JUN-2000.
XX
XX PF 18-SEP-1992; 99EP-00124345.
XX
XX PR 18-SEP-1991; 91JP-00238375.
XX PR 18-SEP-1992; 92EP-00116026.
XX
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
XX
XX DR WPI; 2000-402204/35.
XX DR N-PSDB; AAAS1004.
XX
XX PT New humanized chimera antibody KM-871 useful for treating cancer,
XX PT comprises variable region of mouse monoclonal antibody, reactive with
XX PT ganglioside and human antibody constant region.
XX
XX PS Claim 14; Page 28-29; 65pp; English.
XX
XX CC The present sequence is a murine immunoglobulin light chain variable
XX CC region from plasmid KM-641. The coding sequence was used in the creation
XX CC of an expression vector, along with the sequence for a human antibody, to
XX CC produce humanised chimaeric antibodies, which can be used to treat
XX CC cancer. Humanised chimaeric antibodies are more effective than mouse
XX CC antibodies as they do not provoke a reaction in the human and side
XX CC effects, such as the formation of anti-mouse immunoglobulin antibody and
XX CC the rapid half-life of the immunoglobulins, do not occur
XX
XX SQ Sequence 128 AA;

Query Match 100.0%; Score 572; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 4.1e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 80
QY 61 RFSGGSGTDYSLTISNLEPDIATYFCHQYSKLPWTFGGGTTKLEIKR 108
DB 81 RFSGGSGTDYSLTISNLEPDIATYFCHQYSKLPWTFGGGTTKLEIKR 128

RESULT 4
AAB81978
ID AAB81978 standard; protein; 128 AA.
XX
XX AC AAB81978;
XX
XX DT 03-JUL-2001 (first entry)
XX
XX DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 2.
XX
XX KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX KW cancer.
XX
XX OS Mus musculus.
XX
XX PN WO200123432-A1.
XX
XX PD 05-APR-2001.
XX
XX PF 29-SEP-2000; 2000WO-JP006774.
XX
XX PR 30-SEP-1999; 99JP-00278291.
XX PR 06-APR-2000; 2000JP-00105088.
XX
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX DR WPI; 2001-266143/27.

XX
XX PT New human type complementation-determining region-transplanted antibody
XX PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX PT of e.g. tumors, with low antigenicity, little side effects but potent
XX PT activity in cancer.
XX
XX PS Example 1; Page 140; 183pp; Japanese.
XX
XX CC The present invention describes a monoclonal antibody which can react
XX CC specifically with ganglioside GD3. The antibody and its derivatives are
XX CC useful in the diagnosis and therapy of tumours, particularly cancer
XX CC diagnosis. The present sequence is a protein used in the exemplification
XX CC of the invention
XX
XX SQ Sequence 128 AA;

Query Match 100.0%; Score 572; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 4.1e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 80
QY 61 RFSGGSGTDYSLTISNLEPDIATYFCHQYSKLPWTFGGGTTKLEIKR 108
DB 81 RFSGGSGTDYSLTISNLEPDIATYFCHQYSKLPWTFGGGTTKLEIKR 128

RESULT 5
ABU11003
ID ABU11003 standard; protein; 128 AA.
XX
XX AC ABU11003;
XX
XX DT 04-FEB-2003 (first entry)
XX
XX DE Modified ganglioside GD3 antibody associated protein #2.
XX
XX KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
XX OS Mus musculus.
XX
XX PN WO200278739-A1.
XX
XX PD 10-OCT-2002.
XX
XX PF 29-MAR-2002; 2002WO-JP003170.
XX
XX PR 29-MAR-2001; 2001JP-00097483.
XX
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX PI Shitara K, Niwa R, Kanazawa J, Asada M;
XX
XX DR WPI; 2003-067410/06.
XX
XX PT Drugs containing genetically-modified antibody against ganglioside GD3,
XX PT its fragment, immunocompetent cell activators or/and anticancer agents in
XX PT combination, applicable in treating malignant tumor like melanoma.
XX
XX PS Example 3; Page 98; 121pp; Japanese.
XX
XX CC The invention describes drugs contain a genetically-modified antibody
XX CC against ganglioside GD3 or its fragment and at least 1 of a substance
XX CC capable of activating immunocompetent cells and a substance having an
XX CC anticancer activity in combination. The drugs can be used to treat tumor
XX CC like melanoma and can provide a treatment with enhanced therapeutic
XX CC effect and little side-reactions, particularly to relieve problems of
XX CC side-effects during the conventional single administration. This sequence
XX CC represents a protein associated with the anti- ganglioside GD3 antibody
XX
XX SQ Sequence 128 AA;

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```
Query Match      100.0%; Score 572; DB 6; Length 128;
Best Local Similarity 100.0%; Pred. No. 4.1e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
   |||||
DB 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 80
   |||||

QY 61 RPSGGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGGKLEIKR 108
   |||||
DB 81 RPSGGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGGKLEIKR 128
   |||||

RESULT 6
AA28368
ID AAY28368 standard; protein; 128 AA.
XX
AC AAY28368;
XX
DT 04-NOV-1999 (first entry)
XX
DE pKM641 LA2 immunoglobulin light chain.
XX
KW antibody; nucleotide; genomic; hypervariable region; chimeric;
KW light chain; amino acid.
XX
OS Mus sp.
XX
PN US5939532-A.
XX
PD 17-AUG-1999.
XX
PF 07-JUN-1995; 95US-00483528.
XX
PR 07-SEP-1993; 93US-00116778.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;
DR WPI; 1999-468416/39.
DR N-PSDB; AAX99481.
XX
PT Chimeric human antibody expression vectors.
XX
PS Example 1; Col 99; 188pp; English.
XX
CC This immunoglobulin region was isolated from pKM641LA2, A methionine
CC codon, presumably the initiation codon ATG, was found in the vicinity of
CC the 5' terminus and the sequence has a full length leader sequence. The
CC chimeric human antibodies are useful in the treatment of cancer,
CC especially that which is of neural ectodermal origin. In contrast to
CC prior art constructs based on mouse monoclonal antibodies, the chimeric
CC human antibodies do not cause anti-mouse immunoglobulin production. The
CC chimeric human antibodies have a prolonged half-life and a reduced
CC frequency of adverse effects when compared to mouse monoclonal antibodies
XX
SQ Sequence 128 AA;

Query Match      98.6%; Score 564; DB 2; Length 128;
Best Local Similarity 99.1%; Pred. No. 1.8e-38;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
   |||||
DB 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 80
   |||||

QY 61 RPSGGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGGKLEIKR 108
   |||||
DB 81 RPSGGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGGKLEIKR 128
   |||||

RESULT 7
AAR33257
ID AAR33257 standard; protein; 128 AA.
XX
AC AAR33257;
XX
DT 25-MAR-2003 (revised)
DT 12-JUL-1993 (first entry)
XX
DE Rat immunoglobulin L chain variable region of pKM641LA2.
XX
KW Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;
KW humanised; chimeric; antibody; expression vector.
XX
OS Rattus rattus.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "Signal peptide"
FT Protein 21..128
FT /note= "Mature protein"
XX
PN EP533199-A2.
XX
PD 24-MAR-1993.
XX
PF 18-SEP-1992; 92EP-00116026.
XX
PR 18-SEP-1991; 91JP-00238375.
XX
PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.
XX
PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
DR WPI; 1993-095510/12.
DR N-PSDB; AAR33258.
XX
PT Humanised chimeric antibody prodn. against ganglioside GD3 - for treating
PT cancers, such as melanoma, neuroblastoma, etc.
XX
PS Claim 6; Page 30-31; 63pp; English.
XX
CC The sequences given in AAR33256-57 represent rat heavy and light chain
CC variable regions respectively. The DNA sequences encoding these proteins
CC were used in the construction of humanised chimeric antibody expression
CC vectors. In these humanised antibodies none of the amino acids of the non
CC -human animal Ab variable region have been changed. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 128 AA;

Query Match      98.3%; Score 562; DB 2; Length 128;
Best Local Similarity 99.1%; Pred. No. 2.7e-38;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60
   |||||
DB 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 80
   |||||

QY 61 RPSGGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGGKLEIKR 108
   |||||
DB 81 RPSGGSGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGGKLEIKR 128
   |||||

RESULT 8
AAR53340
ID AAR53340 standard; protein; 128 AA.
XX
AC AAR53340;
XX
DT 18-NOV-1994 (first entry)
XX
DE KM641 H chain variable region.
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XX Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;
KW expression vector; heavy; light; chain; hypervariable region; CDR;
KW constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.
XX Mus musculus.
XX Key Location/Qualifiers
FH Peptide 1..20
FT /label= sig_peptide
XX AU9346181-A.
XX 17-MAR-1994.
XX 07-SEP-1993; 93AU-00046181.
XX 07-SEP-1992; 92JP-00238452.
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;
XX WPI; 1994-126857/16.
XX N-PSDB; AAQ45438.
XX Humanised antibody specific for ganglioside GM2 - used for producing a
XX cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.
XX Example 2; Page 115-116; 191pp; English.
XX Example 2 describes the construction of the vector pCh1641HA1 for
XX chimeric human antibody H chain expression. mRNA from mouse anti-CD3
XX monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain
XX cDNAs isolated. The base sequences of the Ig variable regions in KM641 H
XX chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in
XX AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector
XX was constructed by joining the H chain variable region gene from
XX pKM641HA3 to a vector for chimeric human Ab H chain expression using the
XX synthetic DNAs given in AAQ63439 and AAQ63440
XX Sequence 128 AA;
XX Query Match 97.4%; Score 557; DB 2; Length 128;
XX Best Local Similarity 98.1%; Pred. No. 6.8e-38;
XX Matches 106; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQMTQTASSLPASLGDRTVITSCASQDISNYLNWYQQKPDGTGTVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQTASSLPASLGDRTVITSCASQDISNYLNWYQQKPDGTGTVKLLIFYSSNLHSGVPS 80
QY 61 RPSGGSGTDYSLTISNLEPEDATYFCHQYSKLPMTFGGKLEIKR 108
DB 81 RPSGGSGTDYSLTISNLEPEDATYFCHQYSKLPMTFGGKLEIKR 128
RESULT 9
AAW00834
ID AAW00834 standard; protein; 108 AA.
AC AAW00834;
XX 20-MAY-1997 (first entry)
XX Variable light chain of anti-human Fas ligand antibody NOK-1.
XX Variable region; light chain; human; Fas ligand; monoclonal; antibody;
KW NOK-1; hybridoma; inhibition; apoptosis; assay; diagnosis; disease;
KW hepatitis; infectious mononucleosis; systemic lupus erythematosus.
XX Mus musculus.
XX WO9629350-A1.

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XX 26-SBP-1996.
XX 21-MAR-1996; 96WO-JP000734.
XX 20-MAR-1995; 95JP-00087420.
XX 27-OCT-1995; 95JP-00303492.
XX (SUME ) SUMITOMO ELECTRIC IND CO.
XX Kayagaki N, Yagita H, Okumura K, Nakata M;
XX WPI; 1996-443140/44.
XX N-PSDB; AAT39560.
XX Monoclonal antibody specifically recognising the Fas ligand - useful for
XX the detection of Fas ligands either on cell surface or in solution.
XX Claim 41; Page 93-94; 133pp; Japanese.
XX The present sequence is the light chain variable region of the anti-human
XX Fas ligand monoclonal antibody (Mab) NOK-1. NOK-1 is produced by the
XX hybridoma NOK-1 (PERM BP-5044), which was prepared by immunising mice
XX with transformed human Fas ligand expressing COS cells, and fusing spleen
XX cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580)
XX cells. The Mab recognises the human Fas ligand on the cell surface or in
XX solution, and can be used to inhibit the apoptosis inducing cell surface
XX Fas ligand/Fas reaction. The Mab can also be used for a Fas ligand assay
XX in biological samples (e.g. human blood), especially for disease
XX diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus
XX erythematosus
XX Sequence 108 AA;
XX Query Match 91.1%; Score 521; DB 2; Length 108;
XX Best Local Similarity 90.7%; Pred. No. 4.9e-35;
XX Matches 98; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQTASSLPASLGDRTVITSCASQDISNYLNWYQQKPDGTGTVKLLIFYSSNLHSGVPS 60
DB 1 DIQMTQTSSLSASLGDRTVITSCASQDISNYLNWYQQKPDGTGTVKLLIYTSRLHSGVPS 60
QY 61 RPSGGSGTDYSLTISNLEPEDATYFCHQYSKLPMTFGGKLEIKR 108
DB 61 RPSGGSGTDYSLTISNLEPEDATYFCHQYSEFPWTFGGKLEIKR 108
RESULT 10
AAR12359
ID AAR12359 standard; protein; 127 AA.
XX AAR12359;
XX 25-MAR-2003 (revised)
XX 15-AUG-1991 (first entry)
XX Light (kappa) chain variable region of murine 1C11 immunoglobulin.
XX Chimeric antibodies; immunoconjugates; HIV; AIDS.
XX Mus musculus.
XX WO9107493-A.
XX 30-MAY-1991.
XX 13-NOV-1989; 89US-00433730.
XX 13-NOV-1989; 89US-00433730.
XX (XOMA ) XOMA CORP.
XX (GEC ) GREEN CROSS CORP.

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PI Better MD, Horwitz AH, Ghoshdasti P, Robinson R;  
XX WPI; 1991-178105/24.  
DR N-PSDB; AAQ12061.  
XX New chimeric mouse-human antibodies - used to detect, kill and remove HIV  
PT -1 antigen from sample.  
XX Disclosure; Fig 13; 107pp; English.  
XX This is the light (kappa)- chain variable (V) region of a mouse  
CC monoclonal antibody (MAB), 1C11, and is specific for an HIV-1 viral  
CC antigen. It is used in the construction of a chimeric MAB comprising  
CC heavy and light chains having murine V regions and human C regions. The  
CC chimeric MABs are more effective than murine MAB 1C11 since they have an  
CC increased compatibility in humans. The heavy and light chain V-regions  
CC are joined by manipulating their respective joining (J) regions, to  
CC generate restriction enzyme recognition sites. The chimeric MABs can be  
CC used as immunoconjugates, in association with e.g. toxins for HIV  
CC treatment. They can also be used in diagnosis of HIV. See also AAQ12056-  
CC 60 and AAQ12062-63. (Updated on 25-MAR-2003 to correct PA field.)  
CC (Updated on 25-MAR-2003 to correct PI field.) (Updated on 25-MAR-2003 to  
CC correct DR field.)  
XX Sequence 127 AA;  
SQ  
Query Match 90.9%; Score 520; DB 2; Length 127;  
Best Local Similarity 91.6%; Pred. No. 7e-35;  
Matches 98; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60  
DB 21 DIQMTQTSSLSASLGDRVTISCSASQGISNYLNWYQKPDGTVKLLIYTTSLHSGVPS 80  
QY 61 RFSGGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGKLEIK 107  
DB 81 RFSGGSGTDYSLTISNLEPEDIAFYCCQYSKLPWTFGGKLEIK 127  
RESULT 11  
AAW04177  
ID AAW04177 standard; protein; 108 AA.  
AC AAW04177;  
XX  
XX 19-MAY-1997 (first entry)  
DE Variant variable light chain of Fas ligand antibody NOK-1.  
XX  
XX Variable region; light chain; human; Fas ligand; monoclonal; antibody;  
KW NOK-1; hybridoma; inhibition; apoptosis; assay; diagnosis; disease;  
KW hepatitis; infectious mononucleosis; systemic lupus erythematosus;  
KW variant.  
XX  
XX Mus musculus.  
OS  
XX WO9629350-A1.  
PN  
XX 26-SEP-1996.  
PD  
XX 21-MAR-1996; 96WO-JP000734.  
PF  
XX 20-MAR-1995; 95JP-00087420.  
PR  
XX 27-OCT-1995; 95JP-00303492.  
XX (SUME ) SUMITOMO ELECTRIC IND CO.  
PA  
XX Kayagaki N, Yagita H, Okumura K, Nakata M;  
XX WPI; 1996-443140/44.  
DR N-PSDB; AAT39550.  
XX Monoclonal antibody specifically recognising the Fas ligand - useful for

PT the detection of Fas ligands either on cell surface or in solution.  
XX Claim 20; Page 80-81; 133pp; Japanese.  
XX The present sequence is a variant light chain variable region of the anti  
CC -human Fas ligand monoclonal antibody (MAB) NOK-1. NOK-1 is produced by  
CC the hybridoma NOK-1 (FERM BP-5044), which was prepared by immunising mice  
CC with transformed human Fas ligand expressing COS cells, and fusing spleen  
CC cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580)  
CC cells. The MAB recognises the human Fas ligand on the cell surface or in  
CC solution, and can be used to inhibit the apoptosis inducing cell surface  
CC Fas ligand/Fas reaction. The MAB can also be used for a Fas ligand assay  
CC in biological samples (e.g. human blood), especially for disease  
CC diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus  
CC erythematosus  
XX  
SQ Sequence 108 AA;  
Query Match 90.2%; Score 516; DB 2; Length 108;  
Best Local Similarity 89.8%; Pred. No. 1.3e-34;  
Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60  
DB 1 DIQMTQSPSSLSASLGDRVTISCRASQDISNYLNWYQKPDGTVKLLIYTTSLHSGVPS 60  
QY 61 RFSGGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGKLEIKR 108  
DB 61 RFSGGSGTDYSLTISNLEPEDIAFYCCQYSEFPWTFGGGKLEIKR 108  
RESULT 12  
AAW16620  
ID AAW16620 standard; protein; 108 AA.  
XX  
XX AAW16620;  
XX  
XX 14-JAN-1998 (first entry)  
DE Anti-human FasL antibody (NOK1) light chain variable region.  
XX  
XX Light chain; variable region; mouse; murine; human; Fas ligand; FasL;  
KW monoclonal antibody; MAB; hybridoma; treatment; hepatitis;  
KW hepatitis B virus; HBV; hepatitis C virus; HCV; apoptosis; liver cell;  
KW glutamate oxaloacetate; pyruvate transaminase.  
XX  
XX Mus sp.  
OS  
XX WO9715326-A1.  
PN  
XX 01-MAY-1997.  
PD  
XX 24-OCT-1996; 96WO-JP003089.  
PF  
XX 27-OCT-1995; 95JP-00303491.  
PR  
XX (SUME ) SUMITOMO ELECTRIC IND CO.  
PA  
XX Seino K, Kayagaki N, Yagita H, Okumura K, Nakata M;  
XX WPI; 1997-258767/23.  
DR N-PSDB; AAT66710.  
XX  
XX Anti-human Fas Ligand antibody to treat hepatitis - controls apoptosis in  
PT liver cells and improves liver function.  
XX  
XX Claim 6; Page 30-31; 51pp; Japanese.  
XX The present sequence is the light chain variable region of the murine  
CC anti-human Fas ligand (FasL) monoclonal antibody (MAB) NOK1, which is  
CC expressed by the hybridoma NOK1 (FERM BP-5044). The MAB can be used in  
CC the preparation of a composition for the effective oral or parenteral  
CC treatment of hepatitis, including hepatitis caused by hepatitis B or C



CC bone marrow and/or stem cell-enriched peripheral blood cells of the  
CC donor, where the CD7-bearing cell population in (a) and/or the transplant  
CC in (b) are treated with a T-cell depleting effective amount of the fusion  
CC protein or therapeutic composition comprising the fusion protein; and (c)  
CC introducing the transplant into the animal  
XX  
XX

Sequence 650 AA;

Query Match 90.2%; Score 516; DB 6; Length 650;  
Best Local Similarity 90.7%; Pred. No. 7.5e-34;  
Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRTVITSCSASQDISNLYNMYQKPDGTVKLLIFYSSNLHSGVPS 60

Db 17 DIQMTQTSSLSASLGDRTVITSCSASQGISNLYNMYQKPDGTVKLLIYTSLSLHSGVPS 76

QY 61 RFSGGSGTDYSLTISNLEPEDIAFYCHQYKSLPWTFGGKLEIKR 108

Db 77 RFSGGSGTDYSLTISNLEPEDIAFYCHQYKSLPWTFGGKLEIKR 124

RESULT 15

ABR62590

ID ABR62590 standard; protein; 651 AA.

XX AC ABR62590;

XX DT 06-NOV-2003 (first entry)

DE Anti-CD7 antibody TH-69 scFv-Pseudomonas exotoxin A fusion protein.

XX CD7; antibody; TH-69; scFv; exotoxin A; immunotoxin; cytostatic;

KW immunosuppressive; vaccine.

XX Mus sp.

OS Pseudomonas sp.

OS Synthetic.

OS Chimeric.

XX FH Key Location/Qualifiers

FT Region 7..265

FT /label= scFv

FT Region 125..285

FT /label= Linker

FT Region 286..646

FT /label= ETA

XX WO2003051926-A2.

XX PD 26-JUN-2003.

XX PF 11-DEC-2002; 2002WO-EP014064.

XX PR 14-DEC-2001; 2001US-0339422P.

XX PA (UYER-) UNIV ERLANGEN-NUERNBURG.

XX PI Fey GHM, Gramatzki M, Peipp M;

XX DR WPI; 2003-523519/49.

XX DR N-PSDB; ACF05481.

XX New fusion protein comprising functionally linked components of an anti-  
PT CD7 antibody or its fragment and an immunotoxin, useful for treating CD7  
PT positive acute T-cell and/or myeloid leukemias, or Graft-versus-host  
PT disease.  
XX Claim 9; Page 7; 55pp; English.

XX The present sequence is that of a novel fusion protein comprising an scFv  
CC fragment of anti-CD7 monoclonal antibody TH-69 and domains II and III of  
CC Pseudomonas exotoxin A (ETA), joined via a peptide linker, and including  
CC an N-terminal 6xHis tag and C-terminal REDLK sequence. This novel fusion

CC protein binds to CD7-positive T-lymphoid cells and kills them by the  
CC induction of apoptosis. It is an example of anti-CD7 scFv immunotoxin  
CC fusion proteins of the invention. An expression vector, host cells, a  
CC method for producing the fusion protein, and a vaccine comprising the  
CC fusion protein are claimed. The fusion protein is used in the treatment  
CC of disorders involving a hyperproliferation of CD7-positive cells,  
CC especially acute T-cell and/or myeloid leukaemia, and also in the  
CC treatment or prophylaxis of Graft-versus-host disease. A claimed method  
CC of conditioning an animal (e.g. a human) to be transplanted with donor  
CC cells, tissue or organ comprises: (a) depleting the CD7-bearing cell  
CC population in the animal; (b) providing a transplant comprising isolated  
CC bone marrow and/or stem cell-enriched peripheral blood cells of the  
CC donor, where the CD7-bearing cell population in (a) and/or the transplant  
CC in (b) are treated with a T-cell depleting effective amount of the fusion  
CC protein or therapeutic composition comprising the fusion protein; and (c)  
CC introducing the transplant into the animal  
XX

Sequence 651 AA;

Query Match 90.2%; Score 516; DB 6; Length 651;

Best Local Similarity 90.7%; Pred. No. 7.5e-34;

Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRTVITSCSASQDISNLYNMYQKPDGTVKLLIFYSSNLHSGVPS 60

Db 17 DIQMTQTSSLSASLGDRTVITSCSASQGISNLYNMYQKPDGTVKLLIYTSLSLHSGVPS 76

QY 61 RFSGGSGTDYSLTISNLEPEDIAFYCHQYKSLPWTFGGKLEIKR 108

Db 77 RFSGGSGTDYSLTISNLEPEDIAFYCHQYKSLPWTFGGKLEIKR 124

Search completed: August 1, 2005, 09:10:15

Job time : 35.5277 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:59:16 ; Search time 8.1913 Seconds  
(without alignments)  
983.287 Million cell updates/sec

Title: US-10-089-500-56

Perfect score: 572

Sequence: 1 DIQWTQASSLPASLGRVDT.....HOYSKLPWTRGGTKYLEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	100.0	128	4	US-09-225-322B-10
2	572	100.0	128	4	US-09-225-322B-19
3	572	100.0	128	4	US-09-764-304-10
4	572	100.0	128	4	US-09-764-304-19
5	516	90.2	108	3	US-09-065-059-3
6	503	87.9	107	2	US-08-652-558-35
7	502	87.8	111	1	US-08-236-520-2
8	502	87.8	131	5	PCT-US95-05262-2
9	498	87.1	112	3	US-08-487-761-13
10	497	86.9	109	4	US-09-386-658A-4
11	490	85.7	108	4	US-09-232-290-21
12	488	85.3	107	1	US-08-458-516-9
13	488	85.3	127	1	US-08-458-516-5
14	488	85.3	127	3	US-08-649-100-17
15	487	85.1	108	3	US-09-199-149-7
16	487	85.1	274	4	US-09-813-659-30
17	487	85.1	274	4	US-09-549-067A-30
18	487	85.1	302	1	US-08-121-054C-18
19	487	85.1	302	1	US-08-121-054C-30
20	487	85.1	302	3	US-08-539-436-18
21	487	85.1	302	3	US-08-539-436-30
22	487	85.1	302	4	US-09-813-659-18
23	487	85.1	302	4	US-09-813-659-32
24	487	85.1	302	4	US-09-549-067A-18
25	487	85.1	302	4	US-09-549-067A-32
26	484	84.6	109	1	US-07-942-245-10
27	483	84.4	107	2	US-07-934-373C-16
28	483	84.4	107	3	US-08-437-642B-16
29	483	84.4	107	4	US-08-146-206C-16
30	483	84.4	107	4	US-09-705-686-16
31	483	84.4	107	4	US-09-705-392A-16
32	483	84.4	107	4	US-09-705-398-16
33	483	84.4	107	5	PCT-US93-07832-16
34	483	84.4	127	1	US-08-137-117B-37
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36	474	82.9	127	1	US-08-137-117D-29
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39	469	82.0	214	2	US-07-934-373C-24
40	469	82.0	214	3	US-08-437-642B-24
41	469	82.0	214	3	US-08-811-757-1
42	469	82.0	214	3	US-09-249-230-1
43	469	82.0	214	4	US-08-146-206C-24
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45	469	82.0	214	4	US-09-705-392A-24
46	469	82.0	214	5	PCT-US93-07832-24
47	469	82.0	214	5	PCT-US93-07832-24
48	468	81.8	273	2	US-08-403-853-18
49	468	81.5	108	4	US-09-232-290-16
50	464	81.1	127	2	US-08-574-699A-2
51	458	80.1	107	2	US-08-480-434-74
52	458	80.1	107	2	US-08-053-451B-74
53	458	80.1	107	2	US-08-053-451B-176
54	453	79.2	491	4	US-10-011-125A-2
55	451	78.8	109	1	US-07-942-245-11
56	451	78.8	211	4	US-09-170-769A-8
57	449	78.5	110	4	US-09-440-781-94
58	444	77.6	214	1	US-08-458-516-12
59	439.5	76.8	108	1	US-08-202-047-24
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61	439	76.7	107	1	US-08-458-516-8
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63	437	76.4	109	3	US-09-357-710A-21
64	437	76.4	109	4	US-09-357-707-21
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68	433	75.7	127	3	US-08-649-100-33
69	432	75.5	107	2	US-08-652-558-2
70	428	74.8	107	3	US-09-254-189-1
71	427	74.7	110	4	US-09-440-781-95
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78	426	74.5	107	4	US-09-705-686-17
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86	426	74.5	214	3	US-08-437-642B-40
87	426	74.5	214	3	US-09-097-309-2
88	426	74.5	214	3	US-09-097-171A-2
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90	426	74.5	214	4	US-09-940-166A-2
91	426	74.5	214	5	PCT-US93-07832-40
92	426	74.5	233	2	US-07-934-373C-25
93	426	74.5	233	3	US-08-437-642B-25
94	426	74.5	233	4	US-08-146-206C-25
95	426	74.5	233	4	US-09-705-686-25
96	426	74.5	233	4	US-09-705-392A-25
97	426	74.5	233	4	US-09-705-398-25
98	426	74.5	233	5	PCT-US93-07832-25
99	426	74.5	237	3	US-09-097-309-6
100	426	74.5	237	3	US-09-097-171A-10

## ALIGNMENTS

```
RESULT 1
US-09-225-322B-10
; Sequence 10, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cdna KM-641
US-09-225-322B-10
Query Match 100.0%; Score 572; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.8e-51;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASIGDRVTTISCSASQDISNLYNWYQOKPDGTVKLLIFYSSNLHSGVPS 60
Db 21 DIQMTQTASSLPASIGDRVTTISCSASQDISNLYNWYQOKPDGTVKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 108
Db 81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 128

RESULT 2
US-09-225-322B-19
; Sequence 19, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cdna KM-641
US-09-225-322B-19
Query Match 100.0%; Score 572; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.8e-51;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASIGDRVTTISCSASQDISNLYNWYQOKPDGTVKLLIFYSSNLHSGVPS 60
Db 21 DIQMTQTASSLPASIGDRVTTISCSASQDISNLYNWYQOKPDGTVKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 108
Db 81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 128

RESULT 3
US-09-764-304-10
; Sequence 10, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cdna KM-641
US-09-764-304-10
Query Match 100.0%; Score 572; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.8e-51;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASIGDRVTTISCSASQDISNLYNWYQOKPDGTVKLLIFYSSNLHSGVPS 60
Db 21 DIQMTQTASSLPASIGDRVTTISCSASQDISNLYNWYQOKPDGTVKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 108
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Db 81 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKEIKR 128

## RESULT 4

US-09-764-304-19  
; Sequence 19, Application US/09764304  
; Patent No. 6495866  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KOWANA, YOSHIIISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/764.304  
; CURRENT FILING DATE: 2001-01-19  
; EARLIER APPLICATION NUMBER: 09/225,322  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER APPLICATION NUMBER: US 08/454,680  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER APPLICATION NUMBER: US 08/408,133  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER APPLICATION NUMBER: US 08/292,178  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; EARLIER FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: light chain  
; OTHER INFORMATION: variable region  
US-09-764-304-19

Query Match 100.0%; Score 572; DB 4; Length 128;  
Best Local Similarity 100.0%; Pred. No. 3.8e-51;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60  
Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 80  
QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKEIKR 108  
Db 81 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKEIKR 128

## RESULT 5

US-09-065-059-3  
; Sequence 3, Application US/09065059  
; Patent No. 6068841  
; GENERAL INFORMATION:  
; APPLICANT: SEINO, Ken-ichiro  
; APPLICANT: KAVAGAKI, No. 6068841uhiko  
; APPLICANT: YAGITA, Hideo  
; APPLICANT: OKUMURA, Ko  
; APPLICANT: NAKATA, Motomi  
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDermott, Will & Emery  
; STREET: 99 Canal Center Plaza  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/065,059  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bucca Ph.D., Daniel  
; REGISTRATION NUMBER: P-42,368  
; REFERENCE/DOCKET NUMBER: 50356-151  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-518-5100  
; TELEFAX: 703-684-1124  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-065-059-3

Query Match 90.2%; Score 516; DB 3; Length 108;  
Best Local Similarity 89.8%; Pred. No. 1.6e-45;  
Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60  
Db 1 DIQMTQSPSSLSASLGDRVTISCRASQDISNYLNWYQOKPDGTVKLLIYTSRLHSGVPS 60  
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Db 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKEIKR 108

## RESULT 6

US-08-652-558-35  
; Sequence 35, Application US/08652558  
; Patent No. 5861155  
; GENERAL INFORMATION:  
; APPLICANT: LIN, AUGUSTINE YEE-THARN  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER & WITCOFF  
; STREET: 75 STATE STREET, 23RD FLOOR  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,558  
; FILING DATE: JUNE 6, 1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/IB94/00387  
; FILING DATE: NOVEMBER 21, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YANKWICH, LEON R.  
; REGISTRATION NUMBER: 30,237  
; REFERENCE/DOCKET NUMBER: 95,497-L  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-345-9100  
; TELEFAX: 617-345-9111  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 107 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-652-558-35

Query Match 87.8%; Score 503; DB 2; Length 107;  
Best Local Similarity 89.7%; Pred. No. 3.5e-44;  
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSNLHSGVPS 60  
DB 1 DIQMTQTSSLSASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIYTSRLHSGVPS 60

QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIK 107  
DB 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIK 107

RESULT 7  
US-08-236-520-2  
; Sequence 2, Application US/08236520  
; Patent No. 5591629

GENERAL INFORMATION:  
; APPLICANT: Rodriguez, Moses  
; APPLICANT: Miller, David J.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE  
; TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,520  
; FILING DATE: 29-APR-1994  
; CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 27,227  
; REFERENCE/DOCKET NUMBER: MMV92-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-236-520-2

Query Match 87.8%; Score 502; DB 1; Length 131;  
Best Local Similarity 88.9%; Pred. No. 5.6e-44;  
Matches 96; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSNLHSGVPS 60  
DB 21 DIQMTQTSSLSASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIYTSRLHSGVPS 80

QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIK 108  
DB 81 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIK 128

RESULT 8  
PCT-US95-05262-2  
; Sequence 2, Application PC/TUS9505262  
; GENERAL INFORMATION:  
; APPLICANT: Mayo Foundation for Medical Education Research  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE  
; TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/05262  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/236,520  
; FILING DATE: April 29, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 27,227  
; REFERENCE/DOCKET NUMBER: MMV92-01 PCT

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-05262-2

Query Match 87.8%; Score 502; DB 5; Length 131;  
Best Local Similarity 88.9%; Pred. No. 5.6e-44;  
Matches 96; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSNLHSGVPS 60  
DB 21 DIQMTQTSSLSASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIYTSRLHSGVPS 80

QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIK 108  
DB 81 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIK 128

RESULT 9  
US-08-487-761-13  
; Sequence 13, Application US/08487761  
; Patent No. 6217866  
; GENERAL INFORMATION:

APPLICANT: Schlessinger, Joseph  
APPLICANT: Givol, David  
APPLICANT: Bellot, Francoise  
APPLICANT: Kris, Richard  
APPLICANT: Ricca, George A.  
APPLICANT: Cheadle, Christopher  
APPLICANT: South, Victoria J.  
TITLE OF INVENTION: Monoclonal Antibodies Specific to Human  
TITLE OF INVENTION: Epidermal Growth Factor Receptor and Therapeutic Methods  
TITLE OF INVENTION: Employing Same  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Road, 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.1  
SOFTWARE: Word 5.0 (patentin)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,761  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/086,411  
FILING DATE: 29-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Goodman, Rosanne  
REGISTRATION NUMBER: 32,534  
REFERENCE/DOCKET NUMBER: A0207C-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 454-3817  
TELEFAX: (215) 454-3808  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-487-761-13

Query Match 87.1%; Score 498; DB 3; Length 112;  
Best Local Similarity 87.0%; Pred. No. 1.2e-43;  
Matches 94; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
QY 1 DIQMTQTASSLPSASLGRVITISCSASQDISNYLNWYQKPDGTGTVKLLIFYSSNLHSGVPS 60  
DB 1 EIHWTTTSSLSASLGRVITISCSASQDIRNYLNWYQKPDGTGTVKLLIYTTSLHSGVPS 60  
QY 61 RFGSGSGTDYSLTISNLEPEDATYFCHQYSKLPWTFGGTTKLEIKR 108  
DB 61 RFGSGSGTDYSLTISNLEPEDATYFCHQYSKLPWTFGGTTKLEIKR 108

RESULT 10  
US-09-386-658A-4  
Sequence 4, Application US/09386658A  
Patent No. 6593137  
GENERAL INFORMATION:  
APPLICANT: Erlanger, Bernard F.  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES  
FILE REFERENCE: 0575/54182  
CURRENT APPLICATION NUMBER: US/09/386, 658A  
CURRENT FILING DATE: 1999-08-31  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 4  
LENGTH: 109  
TYPE: PRT  
ORGANISM: Mouse  
US-09-386-658A-4

Query Match 86.9%; Score 497; DB 4; Length 109;  
Best Local Similarity 86.4%; Pred. No. 1.5e-43;  
Matches 93; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  
QY 1 DIQMTQTASSLPSASLGRVITISCSASQDISNYLNWYQKPDGTGTVKLLIFYSSNLHSGVPS 60  
DB 1 DIQMTQTSSLSASLGRVITISCSASQDINNYLNWYQKPDGTGTVKLLIYTTSLHSGVPS 60

QY 61 RFGSGSGTDYSLTISNLEPEDATYFCHQYSKLPWTFGGTTKLEIKR 108  
DB 61 RFGSGSGTDYSLTISNLEPEDATYFCHQYSKLPWTFGGTTKLEIKR 108

RESULT 11  
US-09-232-290-21  
Sequence 21, Application US/092322290A  
Patent No. 6815540  
GENERAL INFORMATION:  
APPLICANT: PLUCKTHUN, ANDREAS  
APPLICANT: NIEBA, LARS  
APPLICANT: HONEGGER, ANNEMARIE  
TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH  
FILE REFERENCE: MORPHO/7  
CURRENT APPLICATION NUMBER: US/09/232,290A  
CURRENT FILING DATE: 1999-01-15  
EARLIER APPLICATION NUMBER: PCT/EP96/02230  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 21  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Murine  
US-09-232-290-21

Query Match 85.7%; Score 490; DB 4; Length 108;  
Best Local Similarity 88.9%; Pred. No. 7.5e-43;  
Matches 96; Conservative 2; Mismatches 10; Indels 0; Gaps 0;  
QY 1 DIQMTQTASSLPSASLGRVITISCSASQDISNYLNWYQKPDGTGTVKLLIFYSSNLHSGVPS 60  
DB 1 DIQMTQTSSLSASLGRVITISCSASQDISNYLNWYQKPDGTGTVKLLIYTTSLHSGVPS 60  
QY 61 RFGSGSGTDYSLTISNLEPEDATYFCHQYSKLPWTFGGTTKLEIKR 108  
DB 61 RFGSGSGTDYSLTISNLEPEDATYFCHQYSKLPWTFGGTTKLEIKR 108

RESULT 12  
US-08-458-516-9  
Sequence 9, Application US/08458516  
Patent No. 5777085  
GENERAL INFORMATION:  
APPLICANT: Co, Man Sung  
APPLICANT: Tso, J. Yun  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
TITLE OF INVENTION: GPIIb/IIIa  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,516  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/059,159  
FILING DATE: 03-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-37-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-458-516-9

Query Match 85.3%; Score 488; DB 1; Length 107;  
Best Local Similarity 86.9%; Pred. No. 1.2e-42;  
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;  
QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLSHGVPVS 60  
Db 1 DIQMTQTSSLSASLGDRVTISCRASQDINNLYNWKPDGIVKLLIYVTSLSHGVPVS 60  
QY 61 RPSGGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGTTKLEIK 107  
Db 61 RPSGGSGTDYSLTISNLEQEDIATYFCQOGNTLPWTFGGTTKLEIK 107

RESULT 13  
US-08-458-516-5  
Sequence 5, Application US/08458516  
Patent No. 5777085  
GENERAL INFORMATION:  
APPLICANT: Co, Man Sung  
APPLICANT: Tso, J. Yun  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
TITLE OF INVENTION: GPIIb/IIIa  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESS: William M. Smith  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,516  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/059,159  
FILING DATE: 03-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-37-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 127 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-458-516-5

Query Match 85.3%; Score 488; DB 1; Length 127;  
Best Local Similarity 86.9%; Pred. No. 1.5e-42;  
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLSHGVPVS 60  
Db 21 DIQMTQTSSLSASLGDRVTISCRASQDINNLYNWKPDGIVKLLIYVTSLSHGVPVS 80  
QY 61 RPSGGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGTTKLEIK 107  
Db 81 RPSGGSGTDYSLTISNLEQEDIATYFCQOGNTLPWTFGGTTKLEIK 127

RESULT 14  
US-08-649-100-17  
Sequence 17, Application US/08649100  
Patent No. 6114507  
GENERAL INFORMATION:  
APPLICANT: SHIRAKAWA, KAMON  
APPLICANT: NATUSUE, TOMOKAZU  
APPLICANT: NAGATA, SHIGEKAZU  
APPLICANT: CO, MAN SUNG  
APPLICANT: VASQUEZ, MAXIMILIANO  
TITLE OF INVENTION: ANTI-PAS LIGAND ANTIBODY AND ASSAY  
TITLE OF INVENTION: METHOD USING THE ANTI-PAS LIGAND ANTIBODY  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESS: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/649,100  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY JR, GERALD M  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1110-160  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 127 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-649-100-17

Query Match 85.3%; Score 488; DB 3; Length 127;  
Best Local Similarity 87.9%; Pred. No. 1.5e-42;  
Matches 94; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLSHGVPVS 60  
Db 21 DIQMTQTSSLSASLGDRVTISCRASQDINNLYNWKPDGIVKLLIYVTSLSHGVPVS 80  
QY 61 RPSGGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGTTKLEIK 107  
Db 81 RPSGGSGTDYSLTISNLEQEDIATYFCQOGNTLPWTFGGTTKLEIK 127

RESULT 15  
US-09-199-149-7  
Sequence 7, Application US/09199149  
Patent No. 6160099  
GENERAL INFORMATION:  
APPLICANT: Jonak, Zdenka L.

Search completed: August 1, 2005, 09:20:55  
Job time : 9.19913 secs

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OM protein - protein search, using sw model

Run on: August 1, 2005, 09:02:01 ; Search time 28.4953 Seconds  
(without alignments)  
1476.651 Million cell updates

**Title:** US-10-089-500-56

Perfect score:

Sequence: 1 DIQMTQTASSLPASLGDRV.....HQYSKLPWTFGGGTKLEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0

Maximum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%  
Maximum Match 100%

**Maximum Match 100%**  
**Listing first 100 summaries**

Database : , Published Applications AA:\*

Database : PubMed Applications\_A4:

1:	/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
2:	/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*
3:	/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*
4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp.*
5:	/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*
6:	/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp.*
7:	/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pcp.*
8:	/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
9:	/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pcp.*
10:	/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pcp.*
11:	/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp.*
12:	/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp.*
13:	/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
14:	/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
15:	/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*
16:	/cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pcp.*
17:	/cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pcp.*
18:	/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
19:	/cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pcp.*
20:	/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pcp.*
21:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
22:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	572	100.0	128	9	US-09-764-304-10	Sequence 10, Appl
2	572	100.0	128	9	US-09-764-304-19	Sequence 19, Appl
3	572	100.0	128	14	US-10-265-713-10	Sequence 10, Appl
4	572	100.0	128	14	US-10-265-713-19	Sequence 19, Appl
5	572	100.0	128	14	US-10-166-626-10	Sequence 10, Appl
6	572	100.0	128	14	US-10-166-626-19	Sequence 19, Appl
7	510	89.2	108	9	US-09-056-160B-10	Sequence 10, Appl
8	510	89.2	108	14	US-10-234-671-10	Sequence 10, Appl
9	510	88.2	108	17	US-10-974-591-10	Sequence 10, Appl
10	507	88.6	214	18	US-10-683-815-6	Sequence 6, Appl
11	504	88.1	107	18	US-10-938-992-13	Sequence 13, Appl

85 469 82.0 214 16 US-10-835-641-24  
86 468 81.8 233 16 US-10-660-128-9  
87 465 81.3 247 17 US-10-620-278-23  
88 465 81.3 247 17 US-10-620-049-23  
89 462 80.8 247 15 US-10-620-278-25  
90 462 80.8 247 17 US-10-620-049-25  
91 453 79.2 110 9 US-09-056-160B-103  
92 453 79.2 110 14 US-10-234-671-101  
93 453 79.2 110 17 US-10-974-591-101  
94 453 79.2 237 9 US-09-056-160B-100  
95 453 79.2 237 14 US-10-234-671-100  
96 453 79.2 237 17 US-10-974-591-100  
97 453 79.2 491 13 US-10-011-125-2  
98 452 79.0 108 18 US-10-683-815-19  
99 452 79.0 108 18 US-10-496-869-33  
100 451 78.8 107 9 US-09-056-160B-15

ALIGNMENTS

RESULT 1  
US-09-764-304-10  
; Sequence 10, Application US/09764304  
; Patent No. US20020026036A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUMANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/764,304  
; EARLIER FILING DATE: 2001-01-19  
; EARLIER APPLICATION NUMBER: 09/225,322  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER APPLICATION NUMBER: US 08/454,680  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER APPLICATION NUMBER: US 08/408,133  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER APPLICATION NUMBER: US 08/292,178  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; EARLIER FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: light chain  
; OTHER INFORMATION: variable region  
US-09-764-304-19

Query Match 100.0%; Score 572; DB 9; Length 128;  
Best Local Similarity 100.0%; Pred. No. 3e-45;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DIQMTQTASSLPASLGDRVTITSCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 60  
DB 21 DIQMTQTASSLPASLGDRVTITSCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 80  
QY 61 RFSGGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGKLEIKR 108  
DB 81 RFSGGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGKLEIKR 128  
RESULT 3  
US-10-265-713-10  
; Sequence 10, Application US/10265713  
; Publication No. US20030095964A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUMANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/10/265,713  
; EARLIER FILING DATE: 2002-10-08  
; EARLIER APPLICATION NUMBER: US/09/225,322  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER APPLICATION NUMBER: US 08/454,680  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER APPLICATION NUMBER: US 08/408,133  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER APPLICATION NUMBER: US 08/292,178  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; EARLIER FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: cdna KM-641  
US-09-764-304-10

Query Match 100.0%; Score 572; DB 9; Length 128;  
Best Local Similarity 100.0%; Pred. No. 3e-45;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DIQMTQTASSLPASLGDRVTITSCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 60  
DB 21 DIQMTQTASSLPASLGDRVTITSCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 80  
QY 61 RFSGGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGKLEIKR 108  
DB 81 RFSGGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGKLEIKR 128

RESULT 2  
US-09-764-304-19  
; Sequence 19, Application US/09764304

; Patent No. US20020026036A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUMANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/764,304  
; EARLIER FILING DATE: 2001-01-19  
; EARLIER APPLICATION NUMBER: 09/225,322  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER APPLICATION NUMBER: US 08/454,680  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER APPLICATION NUMBER: US 08/408,133  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER APPLICATION NUMBER: US 08/292,178  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; EARLIER FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: light chain  
; OTHER INFORMATION: variable region  
US-09-764-304-19

Query Match 100.0%; Score 572; DB 9; Length 128;  
Best Local Similarity 100.0%; Pred. No. 3e-45;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DIQMTQTASSLPASLGDRVTITSCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 60  
DB 21 DIQMTQTASSLPASLGDRVTITSCSASQDISNLYNWYQKPDGTVKLLIFYSSNLHSGVPS 80  
QY 61 RFSGGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGKLEIKR 108  
DB 81 RFSGGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGKLEIKR 128  
RESULT 3  
US-10-265-713-10  
; Sequence 10, Application US/10265713  
; Publication No. US20030095964A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUMANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/10/265,713  
; EARLIER FILING DATE: 2002-10-08  
; EARLIER APPLICATION NUMBER: US/09/225,322  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER APPLICATION NUMBER: US 08/454,680  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER APPLICATION NUMBER: US 08/408,133  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER APPLICATION NUMBER: US 08/292,178  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; EARLIER FILING DATE: 1991-09-18

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; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-10

Query Match      100.0%; Score 572; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 3e-45;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGDRVTISCSASQDISNLYNMYQOKPDGTVKLLIFYSSNLHSGVPS 60
    |||||
Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNLYNMYQOKPDGTVKLLIFYSSNLHSGVPS 80
    |||||

Qy 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIKR 108
    |||||
Db 81 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIKR 128
    |||||

RESULT 4
US-10-265-713-19
; Sequence 19, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US 07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: light chain
US-10-265-713-19

Query Match      100.0%; Score 572; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 3e-45;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGDRVTISCSASQDISNLYNMYQOKPDGTVKLLIFYSSNLHSGVPS 60
    |||||
Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNLYNMYQOKPDGTVKLLIFYSSNLHSGVPS 80
    |||||

Qy 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIKR 108
    |||||
Db 81 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIKR 128
    |||||
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RESULT 5
US-10-166-626-10
; Sequence 10, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US 07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-10

Query Match      100.0%; Score 572; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 3e-45;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGDRVTISCSASQDISNLYNMYQOKPDGTVKLLIFYSSNLHSGVPS 60
    |||||
Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNLYNMYQOKPDGTVKLLIFYSSNLHSGVPS 80
    |||||

Qy 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIKR 108
    |||||
Db 81 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGTTKLEIKR 128
    |||||

RESULT 6
US-10-166-626-19
; Sequence 19, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US 07/947,674
; PRIOR FILING DATE: 1992-09-17
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Matches	95;	Conservative	7;	Mismatches	6;	Indels	0;	Gaps	0;
QY	1	DIQMTQTASSLPASLGDRVTISCSASQDISNYLWYQOKPDGTVKLLIFYSSNLHSGVPS	60						
Db	1	DIQMTQTASSLPASLGDRVTISCSASQDISNYLWYQOKPDGTVKLLIFYSSNLHSGVPS	60						
QY	61	RFSGGSGTDYSLTISNLEPDIATYFCHOYSKLPWTFGGGTKLEIKR	108						
Db	61	RFSGGSGTDYSLTISNLEPDIATYFCHOYSKLPWTFGGGTKLEIKR	108						
RESULT 8									
US-10-234-671-10									
; Sequence 10, Application US/10234671									
; Publication No. US20030190317A1									
; GENERAL INFORMATION:									
; APPLICANT: Baca, Manuel									
; Wells, James A.									
; Presta, Leonard G.									
; Lowman, Henry B.									
; Chen, Yvonne M.									
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES									
; NUMBER OF SEQUENCES: 131									
; CORRESPONDENCE ADDRESS:									
; ADDRESSEE: Genentech, Inc.									
; STREET: 1 DNA Way									
; CITY: South San Francisco									
; STATE: California									
; COUNTRY: USA									
; ZIP: 94080									
; COMPUTER READABLE FORM:									
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk									
; COMPUTER: IBM PC compatible									
; OPERATING SYSTEM: PC-DOS/MS-DOS									
; SOFTWARE: WinPatIn (Genentech)									
; CURRENT APPLICATION DATA:									
; APPLICATION NUMBER: US/10/234,671									
; FILING DATE: 03-Sep-2002									
; CLASSIFICATION: <Unknown>									
; PRIOR APPLICATION DATA:									
; APPLICATION NUMBER: 09/056160									
; FILING DATE: 06-APR-1998									
; APPLICATION NUMBER: 60/126446									
; FILING DATE: 07-APR-1997									
; APPLICATION NUMBER: 60/054856									
; FILING DATE: 06-AUG-1997									
; ATTORNEY/AGENT INFORMATION:									
; NAME: Cui, Steven X.									
; REGISTRATION NUMBER: 44,637									
; REFERENCE/DOCKET NUMBER: P1093R2C1									
; TELECOMMUNICATION INFORMATION:									
; TELEPHONE: 650/225-8674									
; TELEFAX: 650/952-9881									
; INFORMATION FOR SEQ ID NO: 10:									
; SEQUENCE CHARACTERISTICS:									
; LENGTH: 108 amino acids									
; TYPE: Amino Acid									
; TOPOLOGY: Linear									
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:									
US-10-234-671-10									
Query Match 89.2%; Score 510; DB 14; Length 108;									
Best Local Similarity 88.0%; Pred. No. 1.4e-39;									
Matches	95;	Conservative	7;	Mismatches	6;	Indels	0;	Gaps	0;
QY	1	DIQMTQTASSLPASLGDRVTISCSASQDISNYLWYQOKPDGTVKLLIFYSSNLHSGVPS	60						
Db	1	DIQMTQTASSLPASLGDRVTISCSASQDISNYLWYQOKPDGTVKLLIFYSSNLHSGVPS	60						
QY	61	RFSGGSGTDYSLTISNLEPDIATYFCHOYSKLPWTFGGGTKLEIKR	108						
Db	61	RFSGGSGTDYSLTISNLEPDIATYFCHOYSKLPWTFGGGTKLEIKR	108						
Query Match 89.2%; Score 510; DB 9; Length 108;									
Best Local Similarity 88.0%; Pred. No. 1.4e-39;									

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RESULT 9
US-10-974-591-10
; Sequence 10, Application US/10974591
; Publication No. US20050112126A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA: US/10/974,591
; APPLICATION NUMBER: US/10/974,591
; FILING DATE: 26-Oct-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/723752
; FILING DATE: 27-Nov-2000
; APPLICATION NUMBER: 08/908469
; FILING DATE: 06-AUG-1997
; APPLICATION NUMBER: 08/833504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-974-591-10
Query Match 89.2%; Score 510; DB 17; Length 108;
Best Local Similarity 88.0%; Pred. No. 1.4e-39;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
Qy 1 DIQMTQTASSLPASIGDRVTISCSASQDISNLYLNWYQOKPDGTGTVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQTSSLSASLGDRVTISCSASQDISNLYLNWYQOKPDGTGTVKLLIYFSSNLHSGVPS 60
Qy 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFFGGTKLEIKR 108
Db 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFFGGTKLEIKR 108
RESULT 10
US-10-683-815-6
; Sequence 6, Application US/10683815
; Publication No. US20040146512A1
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; LEVKOWITZ, Gil
; TITLE OF INVENTION: METHODS OF TREATING ALZHEIMER'S DISEASE
; USING ANTIBODIES DIRECTED AGAINST AMYLOID BETA PEPTIDE AND
; SEQUENCE 21, Application US/08779784
; Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; O'Keefe, Theresa
; Obar, Robert
; TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
; FILE REFERENCE: 3258.1033-001
; CURRENT APPLICATION NUMBER: US/10/938,992
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: 60/502,568
; PRIOR FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-938-992-13
Query Match 88.1%; Score 504; DB 18; Length 107;
Best Local Similarity 86.9%; Pred. No. 4.9e-39;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
Qy 1 DIQMTQTASSLPASIGDRVTISCSASQDISNLYLNWYQOKPDGTGTVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQTSSLSASLGDRVTISCSASRGINNYLNWYQOKPDGTGTVKFLIYFSSNLHSGVPS 60
Qy 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFFGGTKLEIK 107
Db 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFFGGTKLEIFK 107
RESULT 12
US-08-779-784-21
; Sequence 21, Application US/08779784
; Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; O'Keefe, Theresa
; Obar, Robert
; TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
; FILE REFERENCE: 3258.1033-001
; CURRENT APPLICATION NUMBER: US/10/938,992
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: 60/502,568
; PRIOR FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-938-992-13
Query Match 88.1%; Score 504; DB 18; Length 107;
Best Local Similarity 86.9%; Pred. No. 4.9e-39;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
Qy 1 DIQMTQTASSLPASIGDRVTISCSASQDISNLYLNWYQOKPDGTGTVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQTSSLSASLGDRVTISCSASRGINNYLNWYQOKPDGTGTVKFLIYFSSNLHSGVPS 60
Qy 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFFGGTKLEIK 107
Db 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFFGGTKLEIFK 107

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GENERAL INFORMATION:  
APPLICANT: Rodriguez, Moses  
APPLICANT: Miller, David J.  
APPLICANT: Asakura, Kunihiko  
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM  
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
FLOOR  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/779,784  
FILING DATE: 07-JAN-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/692,084  
FILING DATE: 08-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/236,520  
FILING DATE: 29-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1139-1-001 CIPA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-779-784-21

Query Match 87.8%; Score 502; DB 8; Length 131;  
Best Local Similarity 88.9%; Pred. No. 9.3e-39;  
Matches 96; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASGLDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60  
DB 21 DIQMTQTSSLSASGLDRVTISCRASQDISNYLNWYQKPDGTVKLLIYTSRLHSGVPS 80

QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 108  
DB 81 RFSGGSGTDYSLTISNLEQEDIATYFCQGNLTPWTFGGGKLEIKR 128

RESULT 13  
US-10-010-729-64  
Sequence 64, Application US/10010729  
Publication No. US20030185827A1  
GENERAL INFORMATION:  
APPLICANT: Rodriguez, Moses  
APPLICANT: Miller, David J.  
APPLICANT: Pease, Larry R.  
TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and  
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous  
TITLE OF INVENTION: System  
FILE REFERENCE: 1199-1-005CIP2  
CURRENT APPLICATION NUMBER: US/10/010,729  
CURRENT FILING DATE: 2004-11-13  
PRIOR APPLICATION NUMBER: 09/730,473

PRIOR FILING DATE: 2000-12-05  
PRIOR APPLICATION NUMBER: 09/580,787  
PRIOR FILING DATE: 2000-05-30  
PRIOR APPLICATION NUMBER: 09/322,862  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 08/779,784  
PRIOR FILING DATE: 1997-01-07  
PRIOR APPLICATION NUMBER: 08/692,084  
PRIOR FILING DATE: 1996-08-08  
PRIOR APPLICATION NUMBER: 08/236,520  
PRIOR FILING DATE: 1994-04-29  
NUMBER OF SEQ ID NOS: 80  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 64  
LENGTH: 131  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-010-729-64

Query Match 87.8%; Score 502; DB 14; Length 131;  
Best Local Similarity 88.9%; Pred. No. 9.3e-39;  
Matches 96; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASGLDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60  
DB 21 DIQMTQTSSLSASGLDRVTISCRASQDISNYLNWYQKPDGTVKLLIYTSRLHSGVPS 80

QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 108  
DB 81 RFSGGSGTDYSLTISNLEQEDIATYFCQGNLTPWTFGGGKLEIKR 128

RESULT 14  
US-10-938-992-17  
Sequence 17, Application US/10938992  
Publication No. US20050152903A1  
GENERAL INFORMATION:  
APPLICANT: Newman, Walter  
APPLICANT: Qin, Shixin  
APPLICANT: O'Keefe, Theresa  
APPLICANT: Obar, Robert  
TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1  
FILE REFERENCE: 3258.1033-001  
CURRENT APPLICATION NUMBER: US/10/938,992  
CURRENT FILING DATE: 2004-09-10  
PRIOR APPLICATION NUMBER: 60/502,568  
PRIOR FILING DATE: 2003-09-11  
NUMBER OF SEQ ID NOS: 76  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-938-992-17

Query Match 86.9%; Score 497; DB 18; Length 107;  
Best Local Similarity 88.8%; Pred. No. 2.2e-38;  
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASGLDRVTISCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60  
DB 1 DIQMTQTSSLSASGLDRVTISCRASQDISNYLNWYQKPDGTVKLLIYTSRLHSGVPS 60

QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 107  
DB 61 RFSGGSGTDYSLTISNLEQEDIATYFCQGNLTPWTFGGGKLEIKR 107

RESULT 15  
US-10-197-080-4  
Sequence 4, Application US/10197080  
Publication No. US20030113940A1  
GENERAL INFORMATION:

; APPLICANT: Erlanger, Bernard F.  
 ; APPLICANT: Sheetz, Michael  
 ; APPLICANT: Brus, Louis  
 ; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NANOTUBES AND RELATED METHODS AND COMPOSITIONS  
 ; FILE REFERENCE: 0575/67096-A  
 ; CURRENT APPLICATION NUMBER: US/10/197,080  
 ; CURRENT FILING DATE: 2002-07-16  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 4  
 ; LENGTH: 109  
 ; TYPE: PRT  
 ; ORGANISM: Mouse  
 ;  
 US-10-197-080-4

Query Match 86.9%; Score 497; DB 14; Length 109;  
 Best Local Similarity 86.1%; Pred. No. 2.2e-38;  
 Matches 93; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  
 Qy 1 DIQMTQTASSLPASLGRVITSCASQDINYNLWYQOKPDGTVKLLIFYSSNLHSGVPS 60  
 Db 1 DIQMTQTSSLSASLGRVITFSCASQDINYNLWYQOKPDGTIKLLIYVTSSLSRSGVPS 60  
 Qy 61 RFGSGSGTDYSLTISNLEPEDATYECQYSKLPWTFGGTKLEIKR 108  
 Db 61 RFGSGSGTDYSLTINNLEPEDATYECQYSRLPFTFGSGTKLEIKR 108

Search completed: August 1, 2005, 09:28:04  
 Job time : 29.4953 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:58:15 ; Search time 6.11574 Seconds  
(without alignments)  
1699.125 Million cell updates/sec

Title: US-10-089-500-56

Perfect score: 572

Sequence: 1 DIQWTQTASSLPASLGRVT.....HQYSKLPWTRGGTGKLEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR.79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	520	90.9	111	2 A38740	Ig kappa chain V r
2	514	89.9	111	2 E38740	Ig kappa chain V r
3	510	89.2	111	2 C38740	Ig kappa chain V r
4	507	88.6	107	2 B49026	Ig kappa chain V r
5	502	87.8	108	2 S69900	Ig kappa chain (cl
6	502	87.8	111	2 G38740	Ig kappa chain V r
7	498	87.1	108	1 KVM573	Ig kappa chain V r
8	495	86.5	122	2 A29380	Ig kappa chain pre
9	493	86.2	108	2 S69303	Ig kappa chain (cl
10	493	86.2	115	2 JLO080	Ig kappa chain pre
11	489	85.5	108	1 KVM5AR	Ig kappa chain pre
12	488	85.3	109	2 PH0888	Ig kappa chain V r
13	488	85.3	126	2 A34904	Ig kappa chain V r
14	485.5	84.9	108	2 S38652	Ig kappa chain V r
15	485	84.8	128	2 A26406	Ig kappa chain V r
16	484.5	84.7	107	2 S69901	Ig kappa chain (cl
17	481	84.1	107	2 A48677	Ig kappa chain V r
18	481	84.1	108	2 S69902	Ig kappa chain (cl
19	480	83.9	108	2 S19970	Ig kappa chain V r
20	478	83.6	107	2 B48677	Ig kappa chain V r
21	478	83.6	107	2 B28044	Ig kappa chain V r
22	475	83.0	107	2 A28044	Ig kappa chain V r
23	475	83.0	127	2 PH1224	Ig kappa chain V r
24	474	82.9	107	2 D48677	Ig kappa chain pre
25	474	82.9	108	2 B26405	Ig kappa chain V r
26	473	82.7	108	2 PLO282	Ig kappa chain V r
27	473	82.7	108	2 C26405	Ig kappa chain V r
28	471.5	82.4	107	2 S69906	Ig kappa chain (cl
29	468	81.8	107	2 S32188	Ig kappa chain V r

30	466	81.5	105	2 PH0087	Ig kappa chain V r
31	462	80.8	107	2 C48677	Ig light chain V-J
32	461	80.6	108	2 S11124	Ig kappa chain V r
33	447	78.1	108	2 B30551	Ig kappa chain V r
34	429	75.0	115	2 A53276	Ig kappa chain V r
35	426	74.5	108	1 KIHUOU	Ig kappa chain V-I
36	421	73.6	93	2 S38564	Ig kappa chain V r
37	419	73.3	129	2 S52789	Ig kappa chain V r
38	408	71.3	108	1 KIHURE	Ig kappa chain V-I
39	408	71.3	127	2 S40367	Ig kappa chain V-J
40	402	70.3	108	2 B49047	Ig kappa chain V r
41	402	70.3	110	2 S44118	Ig kappa chain V-J
42	400	69.9	108	1 KIHUAG	Ig kappa chain V-I
43	399	69.8	108	1 KIHURY	Ig kappa chain V-I
44	399	69.8	131	2 S40352	Ig kappa chain V-J
45	396	69.2	108	2 S19674	Ig kappa chain V r
46	395	69.1	107	2 S36264	Ig lambda chain V
47	395	69.1	139	2 S40365	Ig kappa chain - h
48	394	68.9	130	1 KVM5M4	Ig kappa chain pre
49	391	68.4	108	2 I39154	Ig kappa chain (BR
50	391	68.4	125	2 S40333	Ig kappa chain V-J
51	388	67.8	123	2 S40331	Ig kappa chain - h
52	388	67.8	135	2 S24320	Ig kappa chain pre
53	387.5	67.7	107	2 S36275	Ig lambda chain V
54	387	67.7	106	2 PLO262	Ig kappa chain V r
55	386	67.5	109	2 S31998	Ig kappa chain - h
56	385	67.3	108	1 KIHUWE	Ig kappa chain V-I
57	385	67.3	108	2 S44122	Ig kappa chain V r
58	384	67.1	106	2 PLO260	Ig kappa chain V r
59	384	67.1	111	2 I38740	Ig kappa chain V r
60	384	67.1	129	2 S40317	Ig kappa chain - h
61	384	67.1	230	2 S33161	Ig kappa chain - s
62	383	67.0	108	1 KIHUKU	Ig kappa chain V-I
63	383	67.0	129	2 S40369	Ig kappa chain - h
64	383	67.0	129	2 D32513	Ig kappa chain pre
65	382	66.8	106	2 PLO259	Ig kappa chain V r
66	382	66.8	132	2 S40334	Ig kappa chain - h
67	381	66.6	107	2 S36269	Ig lambda chain V
68	381	66.6	109	2 S31981	Ig kappa chain - h
69	381	66.6	125	2 S40349	Ig kappa chain V-J
70	381	66.6	125	2 S03365	Ig kappa chain - m
71	381	66.6	130	2 S40368	Ig kappa chain - h
72	380	66.4	108	1 KIHULY	Ig kappa chain V-I
73	380	66.4	129	2 S52793	Ig kappa chain V r
74	379.5	66.3	124	2 S40336	Ig kappa chain V-J
75	379	66.3	126	2 S40335	Ig kappa chain V-J
76	378.5	66.2	104	2 S26330	Ig kappa chain V r
77	378	66.1	107	2 S36262	Ig lambda chain V
78	378	66.1	141	2 A49134	Ig kappa chain V-I
79	377	65.9	107	2 PLO270	Ig kappa chain V r
80	377	65.9	108	1 KVM5AA	Ig kappa chain V r
81	377	65.9	127	2 S04574	Ig kappa chain pre
82	375.5	65.6	106	2 FC3997	anti-tetanus toxin
83	375.5	65.6	125	2 S40315	Ig kappa chain - h
84	375	65.6	108	4 B47271	nitrophenyl phosph
85	375	65.6	111	2 B37266	Ig kappa chain V r
86	374	65.4	108	1 KIHUBI	Ig kappa chain V-I
87	374	65.4	108	1 KIHUOU	Ig kappa chain V-I
88	374	65.4	108	1 KIHUWS	Ig kappa chain V-I
89	374	65.4	108	2 S42279	Ig lambda chain V
90	374	65.4	117	2 S42263	Ig kappa chain V r
91	374	65.4	117	2 S43528	Ig kappa chain V r
92	374	65.4	129	1 KIHUKW	Ig kappa chain pre
93	374	65.4	129	2 S32806	Ig kappa chain pre
94	373.5	65.3	106	2 C33936	Ig kappa chain V r
95	373	65.2	109	2 S31979	Ig kappa chain - h
96	373	65.2	117	2 S46371	Ig kappa chain V-J
97	372	65.0	106	2 S03303	Ig kappa chain V r
98	372	65.0	117	2 S46376	Ig kappa chain V-J
99	372	65.0	125	2 S40353	Ig kappa chain V-J
100	372	65.0	125	2 S40316	Ig kappa chain - h



Ig kappa chain V region (MOPC 173) - mouse (tentative sequence)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004  
 C/Accession: A01926  
 R/Schiff, C.; Fougereau, M.  
 Eur. J. Biochem. 59, 525-537, 1975  
 A/Title: Determination of the primary structure of a mouse IgG2a immunoglobulin. Amino-acid sequence of the variable region of the heavy chain.  
 A/Reference number: A01926; MUID:76091934; PMID:812696  
 A/Accession: A01926  
 A/Molecule type: protein  
 A/Residues: 1-108 <SCH>  
 A/Cross-references: UNIPROT:P01643  
 C/Comment: This chain was isolated from a myeloma protein.  
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGH, the subunits associate into larger complexes.  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer  
 F/16-90/Domain: immunoglobulin homology <IMM>  
 F/23-88/Disulfide bonds: #status predicted

Query Match	87.1%;	Score 498;	DB 1;	Length 108;
Best Local Similarity	85.2%;	Pred. No. 1.1e-38;		
Matches	92;	Conservative	9;	Mismatches 7; Indels 0; Gaps 0;
Qy	1	DIQWQTASSLPASLGRVITISCSASQDISNYLNWYQKPDGTVKLLIFYSNLSHGVPS	60	
Db	1	DIQWQTSSLSASLGRVITISCSASQDISNYLNWYQKPDGTVKLLIYTSLSHGVPS	60	
Qy	61	RFSGSGSGTDYSLTISNLEPEDVATYFCHQYSKLPWTFGGGTKLEIKR	108	
Db	61	RFSGSGSGTDYSLTISLZPZBIATYCYQYSKLPRTFGGGTKLEIKR	108	

RESULT 8  
 A29380  
 Ig kappa chain precursor V region (AC-1001) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 21-Jan-2000  
 C/Accession: A29380  
 R/Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.  
 J. Biol. Chem. 262, 13579-13583, 1987  
 A/Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable region of the heavy chain of an anti-lymphoma monoclonal antibody.  
 A/Reference number: A92612; MUID:88007582; PMID:3115981  
 A/Accession: A29380  
 A/Molecule type: mRNA  
 A/Residues: 1-122 <CHE>  
 A/Cross-references: GB:M17160; GB:J02815; NID:G196895; PIDN:AAA38824.1; PID:G196896  
 A/Note: The authors translated the codon TTC for residue 1 as Leu  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/30-104/Domain: immunoglobulin homology <IMM>

Query Match	86.5%;	Score 495;	DB 2;	Length 122;
Best Local Similarity	88.0%;	Pred. No. 2.4e-38;		
Matches	95;	Conservative	3;	Mismatches 10; Indels 0; Gaps 0;
Qy	1	DIQWQTASSLPASLGRVITISCSASQDISNYLNWYQKPDGTVKLLIFYSNLSHGVPS	60	
Db	15	DIQWQTSSLSASLGRVITISCSASQDISNYLNWYQKPDGTVKLLIHYTSLSHGVPS	74	
Qy	61	RFSGSGSGTDYSLTISNLEPEDVATYFCHQYSKLPWTFGGGTKLEIKR	108	
Db	75	RFSGSGSGTDYSLTISNLEQEDVATYFCQGGNTLPWTFGGGTKLEIKR	122	

RESULT 9  
 S69903  
 Ig kappa chain (clone KL2.29 / KL2.33 / KL3.8) - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
 C/Accession: S69903; S69904; S69905  
 R/Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.  
 Immunology 75, 116-121, 1992

A>Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin  
A:Reference number: S69900; MUID:92165291; PMID:1537587  
A:Accession: S69903  
A>Status: preliminary; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-108 <WYS>  
A:Cross-references: EMBL:X55044; NID:g511029; PIDN:CAA38884.1; PID:g511030  
A:Accession: S69904  
A>Status: preliminary; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-108 <WY2>  
A:Cross-references: EMBL:X55045; NID:g511031; PIDN:CAA38885.1; PID:g511032  
A:Accession: S69905  
A>Status: preliminary; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-108 <WY3>  
A:Cross-references: EMBL:X55046; NID:g511033; PIDN:CAA38886.1; PID:g511034  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>  
  
Query Match 86.2%; Score 493; DB 2; Length 108;  
Best Local Similarity 88.0%; Pred. No. 3.1e-38;  
Matches 95; Conservative 4; Mismatches 9; Indels 0; Gaps 0;  
  
QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60  
DB 1 DIQMTQTSSLSASLGDRVTISCRASQDISNYLNWYQOKPDGTVKLLIYYTSRLHSGVPS 60  
  
QY 61 RFSGGSGGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGGTKLEIKR 108  
DB 61 RFSGGSGGTDYSLTISNLEQEDIATYFCQGNTPVTFGGGTKLEIKR 108  
  
RESULT 10  
JL0080  
Ig kappa chain precursor V region (anti-phenyloxazolone, 18C10) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 21-Jan-2000  
C:Accession: JL0080  
R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.  
Mol. Immunol. 25, 859-865, 1988  
A>Title: Combinatorial association of V genes: one VH gene codes for three non-cross-reactive V regions  
A:Reference number: JL0076; MUID:89096973; PMID:3211160  
A:Accession: JL0080  
A:Molecule type: mRNA  
A:Residues: 1-115 <KAA>  
A:Cross-references: GB:M2793; NID:g197161; PIDN:AAA38937.1; PID:g197162  
A>Note: the authors translated the codon AGG for residue 30 as Ser  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:1-6/Domain: signal sequence (fragment) #status predicted <SIG>  
F:7-115/Product: Ig light chain #status predicted <MAT>  
F:22-96/Domain: immunoglobulin homology <IMM>  
F:30-40/Region: complementarity-determining 1  
F:56-62/Region: complementarity-determining 2  
  
Query Match 86.2%; Score 493; DB 2; Length 115;  
Best Local Similarity 88.0%; Pred. No. 3.4e-38;  
Matches 95; Conservative 4; Mismatches 9; Indels 0; Gaps 0;  
  
QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60  
DB 7 DIQMTQTSSLSASLGDRVTISCRASQDISNYLNWYQOKPDGTVKLLIYYTSRLHSGVPS 66  
  
QY 61 RFSGGSGGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGGTKLEIKR 108  
DB 67 RFSGGSGGTDYSLTISNLEQEDIATYFCQGNTPVTFGGGTKLEIKR 114  
  
RESULT 11  
KWSAR  
Ig kappa chain V regions (anti-arsenate hybridoma proteins) - mouse  
C:Species: Mus musculus (house mouse)

C>Date: 06-Jul-1982 #sequence\_revision 06-Jul-1982 #text\_change 09-Jul-2004  
C:Accession: A01927  
R:Siegelman, M.; Capra, J.D.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7679-7683, 1981  
A>Title: Complete amino acid sequence of light chain variable regions derived from five non-identical light chain variable regions  
A:Reference number: A01927; MUID:82150934; PMID:6801658  
A:Accession: A01927  
A:Molecule type: protein  
A:Residues: 1-108 <SIE>  
A:Cross-references: UNIPROT:P01644  
A:Experimental source: strain A/J  
A>Note: hp 93G7 differs in having 93-Met; HP 123E6 differs in having 7-Ser, 92-Tyr, and 93-Ala  
A:Comment: The sequence shown is HP R16.7.  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chains held together by two disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger oligomers.  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:16-90/Domain: immunoglobulin homology <IMM>  
F:23-88/Disulfide bonds: #status predicted  
  
Query Match 85.5%; Score 489; DB 1; Length 108;  
Best Local Similarity 88.0%; Pred. No. 7.3e-38;  
Matches 95; Conservative 3; Mismatches 10; Indels 0; Gaps 0;  
  
QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60  
DB 1 DIQMTQTSSLSASLGDRVTISCRASQDISNYLNWYQOKPDGTVKLLIYYTSRLHSGVPS 60  
  
QY 61 RFSGGSGGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGGTKLEIKR 108  
DB 61 RFSGGSGGTDYSLTISNLEQEDIATYFCQGNTPVTFGGGTKLEIKR 108  
  
RESULT 12  
PH0888  
Ig kappa chain V region (anti-CD3) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 21-Jan-2000  
C:Accession: PH0888  
R:Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feidmann, J. Exp. Med. 175, 217-225, 1992  
A>Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocyte antigens  
A:Reference number: PH0885; MUID:92113462; PMID:1346155  
A:Accession: PH0888  
A:Molecule type: mRNA  
A:Residues: 1-109 <SHA>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>  
  
Query Match 85.3%; Score 488; DB 2; Length 109;  
Best Local Similarity 86.1%; Pred. No. 9.1e-38;  
Matches 93; Conservative 4; Mismatches 11; Indels 0; Gaps 0;  
  
QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60  
DB 1 DIQMTQTSSLSASLGDRVTISCRASQDISNYLNWYQOKPDGTVKLLIYYTSRLHSGVPS 60  
  
QY 61 RFSGGSGGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGGTKLEIKR 108  
DB 61 KFSGGSGGTDYSLTISNLEQEDIATYFCQGNTPVTFAGGTKLEIKR 108  
  
RESULT 13  
A34904  
Ig kappa chain precursor V region (5-27) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 09-Jul-2004  
C:Accession: A34904  
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.  
J. Biol. Chem. 265, 133-138, 1990  
A>Title: Active site structure and antigen binding properties of idiotypically cross-reactive

A;Reference number: A34903; MUID:90094387; PMID:2104617  
A;Accession: A34904  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-126 <BED>  
A;Cross-references: UNIPROT:Q91WFB  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;35-109/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 488; DB 2; Length 126;  
Best Local Similarity 86.8%; Pred. No. 1.1e-37;  
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;  
Qy 1 DIQMTOTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60  
Db 20 DIQMTTSSLSASLGDRVTISCRASQDINNLYNWYQOKPDGTVKLLIYTSKLHSGVPS 79  
Qy 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGKLEIK 106  
Db 80 RPSGGSGTDYSLTISNLEQEDIATYFCQGNLTPWTFGGGKLEI 125

## RESULT 14

S38862  
Ig kappa chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: S38862  
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.  
submitted to the EMBL Data Library, August 1993  
A;Description: Production and cloning of TMV-specific monoclonal antibodies.  
A;Reference number: S37200  
A;Accession: S38862  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-108 <FIS>  
A;Cross-references: EMBL:X75854; NID:g429109; PID:g429110  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.9%; Score 485.5; DB 2; Length 108;  
Best Local Similarity 87.0%; Pred. No. 1.1e-37;  
Matches 94; Conservative 4; Mismatches 9; Indels 1; Gaps 1;  
Qy 1 DIQMTOTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60  
Db 1 DVQMTTSSLAASLGDRVTISCRASQDISNYLNWYQOKPDGTVKLLIYTSRLHSGVPS 60  
Qy 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGKLEIK 107  
Db 61 RPSGGSGTDYSLTISNLEQEDIATYFCQGNLTPWTFGGGKLEIK 108

## RESULT 15

A26406  
Ig kappa chain V region (Ars-A) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1991 #text\_change 09-Jul-2004  
C;Accession: A26406  
R;Sanz, I.; Capra, J.D.  
Proc. Natl. Acad. Sci. U.S.A. 84, 1085-1089, 1987  
A;Title: V-K and J-K gene segments of A/J Ars-A antibodies: somatic recombination genera  
A;Reference number: A26406; MUID:87147197; PMID:3103124  
A;Accession: A26406  
A;Molecule type: DNA  
A;Residues: 1-128 <SAN>  
A;Cross-references: UNIPROT:Q91WFB; GB:M15519  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 84.8%; Score 485; DB 2; Length 128;  
Best Local Similarity 87.0%; Pred. No. 2e-37;  
Matches 94; Conservative 4; Mismatches 10; Indels 0; Gaps 0;  
Qy 1 DIQMTOTASSLPASLGDRVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60  
Db 21 DIQMTTSSLSASLGDRVTISCRASQDISNYLNWYQOKPDGTVKLLIYTSRLHSGVPS 80  
Qy 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGKLEIKR 108  
Db 81 RPSGGSGTDYSLTISNLEQEDIATYFCQGNALPRTFGGGKLEIKR 128

Search completed: August 1, 2005, 09:18:45  
Job time : 6.11574 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:55 ; Search time 28.0249 Seconds  
(without alignments)  
1973.408 Million cell updates/sec

Title: US-10-089-500-56

Perfect score: 572

Sequence: 1 DIQMTTASSLPASLGDRVT.....HQVSKLPWTGGTKLEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	87.1	108	1 KV5K MOUSE	P01643 mus musculus
2	489	85.5	108	1 KV5K MOUSE	P01644 mus musculus
3	488	85.3	108	1 KV5L MOUSE	P01645 mus musculus
4	484	84.6	108	1 KV5N MOUSE	P01647 mus musculus
5	481	84.1	108	1 KV5M MOUSE	P01646 mus musculus
6	477	83.4	108	1 KV5O MOUSE	P01648 mus musculus
7	460	80.4	107	2 Q9JL84	Q9JL84 mus musculus
8	458	80.1	108	1 KV5U MOUSE	P01594 mus musculus
9	426	74.5	108	1 KV1B HUMAN	P01496 mus musculus
10	408	71.3	108	1 KV1Q HUMAN	P01594 mus musculus
11	401	70.1	108	1 KV1Y HUMAN	P01594 mus musculus
12	400	69.9	108	1 KV1A HUMAN	P01593 mus musculus
13	399	69.8	108	1 KV1P HUMAN	P01608 mus musculus
14	396	69.2	108	2 Q9JL70	Q9JL70 mus musculus
15	394.5	69.0	107	2 Q96SA9	Q96SA9 mus musculus
16	394	68.9	108	2 Q9JL77	Q9JL77 mus musculus
17	394	68.9	130	1 KV5G MOUSE	P01639 mus musculus
18	394	68.9	236	2 Q6GMX9	Q6GMX9 mus musculus
19	386	67.5	236	2 Q6GMX0	Q6GMX0 mus musculus
20	385	67.3	108	1 KV1R HUMAN	P01610 mus musculus
21	385	67.3	236	2 Q6GMW1	Q6GMW1 mus musculus
22	383	67.0	108	1 KV1L HUMAN	P01604 mus musculus
23	382	66.8	236	2 Q7Z3Y4	Q7Z3Y4 mus musculus
24	382	66.8	244	2 Q65ZC8	Q65ZC8 mus musculus
25	380	66.4	108	1 KV1M HUMAN	P01605 mus musculus
26	379	66.3	236	2 Q6GMX8	Q6GMX8 mus musculus
27	377	65.9	108	1 KV5P MOUSE	P01649 mus musculus
28	377	65.9	240	2 Q65ZC9	Q65ZC9 mus musculus
29	375	65.6	116	2 Q96PF6	Q96PF6 mus musculus
30	375	65.6	236	2 Q6PIH7	Q6PIH7 mus musculus
31	374	65.4	108	1 KV1C HUMAN	P01595 mus musculus

32	374	65.4	108	1 KV1N HUMAN	P01606 mus musculus
33	374	65.4	108	1 KV1S HUMAN	P01611 mus musculus
34	374	65.4	129	1 KV1W HUMAN	P04431 mus musculus
35	371.5	64.9	107	2 Q9UL81	Q9UL81 mus musculus
36	370	64.7	108	1 KV1H HUMAN	P01600 mus musculus
37	370	64.7	108	1 KV1K HUMAN	P01603 mus musculus
38	370	64.7	236	2 Q7TS98	Q7TS98 mus musculus
39	369	64.5	127	2 Q925S9	Q925S9 mus musculus
40	368	64.3	108	1 KV1E HUMAN	P01597 mus musculus
41	368	64.3	108	1 KV1Q HUMAN	P01609 mus musculus
42	368	64.3	108	1 KV1V HUMAN	P04430 mus musculus
43	367	64.2	108	1 KV5S MOUSE	P01652 mus musculus
44	366.5	64.1	109	1 KV1T HUMAN	P01612 mus musculus
45	364.5	63.7	107	1 KV1D HUMAN	P01596 mus musculus
46	361	63.1	108	1 KV1G HUMAN	P01599 mus musculus
47	361	63.1	134	1 KV4C HUMAN	P06314 mus musculus
48	360	62.9	234	2 Q7Z473	Q7Z473 mus musculus
49	359	62.8	108	2 Q9UL79	Q9UL79 mus musculus
50	359	62.8	128	1 KV5E MOUSE	P01637 mus musculus
51	358	62.6	108	1 KV5Q MOUSE	P01650 mus musculus
52	355	62.1	236	2 Q6PIH4	Q6PIH4 mus musculus
53	352	61.5	108	1 KV5T MOUSE	P01653 mus musculus
54	352	61.5	238	2 Q6GJ87	Q6GJ87 mus musculus
55	351	61.4	109	2 Q920E6	Q920E6 mus musculus
56	350.5	61.3	112	2 Q8K1F3	Q8K1F3 mus musculus
57	350.5	61.3	243	2 Q7TQM2	Q7TQM2 mus musculus
58	350	61.2	236	2 Q6PIT5	Q6PIT5 mus musculus
59	349	61.0	129	1 KV1X HUMAN	P04432 mus musculus
60	348.5	60.9	110	1 KV3P MOUSE	P01668 mus musculus
61	347.5	60.8	134	2 Q8VDD0	Q8VDD0 mus musculus
62	347	60.7	108	1 KV5R MOUSE	P01651 mus musculus
63	347	60.7	111	1 KV3O MOUSE	P01667 mus musculus
64	347	60.7	111	1 KV3Q MOUSE	P01669 mus musculus
65	346	60.5	108	1 KV1F HUMAN	P01598 mus musculus
66	345.5	60.4	133	1 KV4B HUMAN	P06313 mus musculus
67	345	60.3	111	1 KV3A MOUSE	P01654 mus musculus
68	345	60.3	114	1 KV4A HUMAN	P01625 mus musculus
69	343	60.0	108	2 Q8VIJ0	Q8VIJ0 mus musculus
70	341	59.6	111	1 KV3C MOUSE	P01656 mus musculus
71	341	59.6	111	1 KV3L MOUSE	P01664 mus musculus
72	341	59.6	111	2 Q920E9	Q920E9 mus musculus
73	339.5	59.4	114	2 Q8K1F1	Q8K1F1 mus musculus
74	337	58.9	111	1 KV3M MOUSE	P01665 mus musculus
75	336	58.7	111	1 KV3D MOUSE	P03977 mus musculus
76	336	58.7	111	1 KV3R MOUSE	P01670 mus musculus
77	336	58.7	131	1 KV3I MOUSE	P01661 mus musculus
78	335	58.6	111	1 KV3H MOUSE	P01660 mus musculus
79	335	58.6	112	1 KV1U HUMAN	P01613 mus musculus
80	335	58.6	117	1 KV1I HUMAN	P01601 mus musculus
81	335	58.6	298	2 Q9QYF0	Q9QYF0 synthetic c
82	334	58.4	112	1 KV3G MOUSE	P01659 mus musculus
83	333	58.2	101	2 Q9JL78	Q9JL78 mus musculus
84	333	58.2	111	1 KV3E MOUSE	P01657 mus musculus
85	332	58.0	111	1 KV3N MOUSE	P01666 mus musculus
86	332	58.0	132	1 KV3F MOUSE	P01658 mus musculus
87	331.5	58.0	109	2 Q9UL78	Q9UL78 mus musculus
88	331.5	58.0	112	2 Q8K1F2	Q8K1F2 mus musculus
89	331.5	58.0	129	1 KV3M HUMAN	P18136 mus musculus
90	331	57.9	111	1 KV3T MOUSE	P01672 mus musculus
91	331	57.9	111	2 Q811U6	Q811U6 mus musculus
92	330.5	57.8	111	2 Q65ZN3	Q65ZN3 mus musculus
93	330	57.7	149	1 KV5A MOUSE	P01633 mus musculus
94	329.5	57.6	113	1 KV2G MOUSE	P01631 mus musculus
95	329	57.5	111	1 KV3S MOUSE	P01671 mus musculus
96	327.5	57.3	241	2 Q921A6	Q921A6 mus musculus
97	327	57.2	103	2 Q9JL80	Q9JL80 mus musculus
98	327	57.2	111	1 KV1J HUMAN	P01662 mus musculus
99	327	57.2	117	1 KV3J HUMAN	P01602 mus musculus
100	325.5	56.9	112	1 KV3B MOUSE	P01655 mus musculus

ALIGNMENTS

```
RESULT 1
KV5J_MOUSE
ID KV5J_MOUSE STANDARD; PRT; 108 AA.
AC P01643;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region MOPC 173.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=76091934; PubMed=812696;
RA Schiff C., Fougereau M.;
RT "Determination of the primary structure of a mouse IGC2a
immunoglobulin. Amino-acid sequence of the light chain.";
RL Eur. J. Biochem. 59:525-537(1975).
CC -|- MISCELLANEOUS: This chain was isolated from a myeloma protein.
DR PIR; A01926; KVM573.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; Igv; 1.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DISULFID 98 108 Framework-4.
FT NON_TER 108 108 By similarity.
SQ SEQUENCE 108 AA; 11819 MW; 2AD29D92A72AA0A3 CRC64;

Query Match 87.1%; Score 498; DB 1; Length 108;
Best Local Similarity 85.2%; Pred. No. 5.4e-43;
Matches 92; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASIGDRVTISCSASQDISNYLWYQKPDGTVKLLIFYSSNLHSGVPS 60
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 DIQMTQTSSLSASLGDRVTISCSASQSIGNYLWYQKPDGTVKLLIYTSLSHSGVPS 60
QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCHOYKSLPWTFGGTTKLEIKR 108
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 RFSGGSGTDYSLTISNLEPEDIATYFCHOYKSLPWTFGGTTKLEIKR 108

RESULT 2
KV5K_MOUSE
ID KV5K_MOUSE STANDARD; PRT; 108 AA.
AC P01644;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP R16.7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsonate antibodies differing
with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -|- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; Igv; 1.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DISULFID 98 108 Framework-4.
FT NON_TER 108 108 By similarity.
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFP58E CRC64;
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```
Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -|- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSP; A01927; KVM5AR.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DISULFID 98 108 Framework-4.
FT NON_TER 108 108 By similarity.
SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFP597 CRC64;

Query Match 85.5%; Score 489; DB 1; Length 108;
Best Local Similarity 88.0%; Pred. No. 4.4e-42;
Matches 95; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASIGDRVTISCSASQDISNYLWYQKPDGTVKLLIFYSSNLHSGVPS 60
DB 1 DIQMTQTSSLSASLGDRVTISCSASQDISNYLWYQKPDGTVKLLIYTSRLHSGVPS 60
QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCHOYKSLPWTFGGTTKLEIKR 108
DB 61 RFSGGSGTDYSLTISNLEPEDIATYFCHOYKSLPWTFGGTTKLEIKR 108

RESULT 3
KV5L_MOUSE
ID KV5L_MOUSE STANDARD; PRT; 108 AA.
AC P01645;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 93G7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsonate antibodies differing
with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -|- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; Igv; 1.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DISULFID 98 108 Framework-4.
FT NON_TER 108 108 By similarity.
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFP58E CRC64;
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Query Match      85.3%; Score 488; DB 1; Length 108;
Best Local Similarity 88.0%; Pred. No. 5.6e-42;
Matches 95; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTOTASSLPASLGRVTVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60
DB 1 DIQMTOTSSLSASLGRVTVTISCSASQDISNYLNWYQOKPDGTVKLLIYTSRLHSGVPS 60

QY 61 RFSGSGSGTDYSLTISNLEPEDATYFCHQYSKLPMTFGGTTKLEIKR 108
DB 61 RFSGSGSGTDYSLTISNLEPEDATYFCHQYSKLPMTFGGTTKLEIKR 108

RESULT 4
KVSM_MOUSE
ID_KVSM_MOUSE STANDARD; PRT; 108 AA.
AC P01647;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 124E1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01594; 1JVS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EF6A2 CRC64;

Query Match      84.6%; Score 484; DB 1; Length 108;
Best Local Similarity 87.0%; Pred. No. 1.4e-41;
Matches 94; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTOTASSLPASLGRVTVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60
DB 1 DIQMTOTSSLSASLGRVTVTISCSASQDISNYLNWYQOKPDGTVKLLIYTSRLHSGVPS 60

QY 61 RFSGSGSGTDYSLTISNLEPEDATYFCHQYSKLPMTFGGTTKLEIKR 108
DB 61 RFSGSGSGTDYSLTISNLEPEDATYFCHQYSKLPMTFGGTTKLEIKR 108

RESULT 5
KVSM_MOUSE
ID_KVSM_MOUSE STANDARD; PRT; 108 AA.
AC P01646;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
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DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 123E6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01594; 1JVS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;

Query Match      84.1%; Score 481; DB 1; Length 108;
Best Local Similarity 87.0%; Pred. No. 2.9e-41;
Matches 94; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTOTASSLPASLGRVTVTISCSASQDISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60
DB 1 DIQMTOTSSLSASLGRVTVTISCSASQDISNYLNWYQOKPDGTVKLLIYTSRLHSGVPS 60

QY 61 RFSGSGSGTDYSLTISNLEPEDATYFCHQYSKLPMTFGGTTKLEIKR 108
DB 61 RFSGSGSGTDYSLTISNLEPEDATYFCHQYSKLPMTFGGTTKLEIKR 108

RESULT 6
KVSO_MOUSE
ID_KVSO_MOUSE STANDARD; PRT; 108 AA.
AC P01648;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 91A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01594; 1JVS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
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```
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34 Framework-1.
FT DOMAIN 35 49 Complementarity-determining-1.
FT DOMAIN 50 56 Framework-2.
FT DOMAIN 57 88 Complementarity-determining-2.
FT DOMAIN 89 97 Framework-3.
FT DOMAIN 98 108 Complementarity-determining-3.
FT DISULFID 23 88 Framework-4.
FT NON_TER 108 108 By similarity.
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5E9A45291C CRC64;

Query Match 83.4%; Score 477; DB 1; Length 108;
Best Local Similarity 85.2%; Pred. No. 7.4e-41;
Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTITSCSASQDISNYLNWYQKPDGTVKLLIFYSNLHSGVPS 60
DB 1 DIQMTQTSSLSASLGDRVTITSCASQDINNLYNRYQKPDGTVKLLIYTSRLHSGVPS 60

QY 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 108
DB 61 RPSGGSGTDYSLTISNLEQEDISTYFCQGNALPRTFGGKLEIKR 108

RESULT 7
Q9JL84 PRELIMINARY; PRT; 107 AA.
AC Q9JL84;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808 (2000).
DR EMBL; AF206022; AAF69320.1; -.
DR HSSP; P01594; 1JVS.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11648 MW; ACF9B1253ACA1E5D CRC64;

Query Match 80.4%; Score 460; DB 2; Length 107;
Best Local Similarity 81.3%; Pred. No. 4e-39;
Matches 87; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTITSCSASQDISNYLNWYQKPDGTVKLLIFYSNLHSGVPS 60
DB 1 DIQMTQTSSLSASLGDRVXXCSASQISNXXWFQKPDGTVKLLIYTSRLHSGVPS 60

QY 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIK 107
DB 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIK 107

us-10-089-500-56.rup

RESULT 8
KV5U_MOUSE STANDARD; PRT; 108 AA.
AC P04946;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Ig kappa chain V-V region NQ5-89.4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IGG response to 2-phenyloxazolone and its early diversification.";
RL Nature 304:320-324 (1983).
CC -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC EMBL; K00745; AAA38690.1; -.
DR HSSP; P01594; 1JVS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Framework-4.
FT DOMAIN 98 107 Complementarity-determining-3.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11866 MW; DB2C885920DC6DDD CRC64;

Query Match 80.1%; Score 458; DB 1; Length 108;
Best Local Similarity 81.5%; Pred. No. 6.4e-39;
Matches 88; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTITSCSASQDISNYLNWYQKPDGTVKLLIFYSNLHSGVPS 60
DB 1 DIQMTQTSSLSASLGHRVTITCSASQDISNYLNWYQKPDGTVKLLIYTSRLHSGVPS 60

QY 61 RPSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKLEIKR 108
DB 61 RPSGGSGATDYSLTITNLQEDXATYXCOQGNLTPYTFGGGKLEIKR 108

RESULT 9
KVIB_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RN      RP      RQ      DB      QY
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN      RP      RQ      DB      QY
RX X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA MEDLINE=7022433; PubMed=1234024;
RA Fehllhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the Bence-
RT Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
RN      RP      RQ      DB      QY
CC -1- MISCELLANEOUS: The structure of the V region was determined by
CC molecular replacement methods using the known structure of the V
CC region of the kappa chain RE1.
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
RN      RP      RQ      DB      QY
CC PIR; A91653; KUHUAU.
DR PDB; 1JY5; X-ray; A=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
RN      RP      RQ      DB      QY
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULPID 23 88
FT STRAND 4 5
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011107ER6F6PB9 CRC64;

Query Match 74.5%; Score 426; DB 1; Length 108;
Best Local Similarity 74.1%; Pred. No. 1.2e-35;
Matches 80; Conservative 12; Mismatches 16; Indels 0; Gaps

1 DIQMTQASSLSPASLGDRTVITCSAQSDISNLYNWYQOKPDGTVKLLIFVSNLHSGVPS
1 DIQMTQSPSLASVGDRTVITTCQASQDISDLYNWYQOKPGKPKLLIYDASNLPSGVPS
61 RFSGGSGSDTYSLTISNLSPEDIATVYCHOYKLPMTFGGTVKLEIKR 108

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Db 61 RFSGGSGAHFTTISLSQPEDATYYQQYDYLPMFTFGGKVEIKR 108

RESULT 10

KV10_HUMAN	STANDARD;	PRT;	108 AA.
ID_KV10_HUMAN			
AC	P01607;		
DC	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	25-OCT-2004 (Rel. 05, Last annotation update)		
DE	Ig kappa chain V-I region Rei.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE.		
RX	MEDLINE=76023758; PubMed=809329;		
RA	Palm W., Hilschmann N.;		
RT	"The primary structure of a crystalline monoclonal immunoglobulin		
RT	kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation		
RT	and characterization of the tryptic peptides; the complete amino acid		
RT	sequence of the protein; a contribution to the elucidation of the		
RT	three-dimensional structure of antibodies, in particular their		
RT	combining site.";		
RL	Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).		
RL	[2]		
RP	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).		
RX	MEDLINE=76039968; PubMed=1182131;		
RA	Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;		
RT	"The molecular structure of a dimer composed of the variable portions		
RT	of the Bence-Jones protein REI refined at 2.0-A resolution.";		
RL	Biochemistry 14:4943-4952(1975).		
CC	-1- MISCELLANEOUS: The C region of this chain has the INV (1,2)		
CC	marker.		
CC	-1- MISCELLANEOUS: This is a Bence-Jones protein.		
CC	PIR; A91663; KIHURE.		
DR	PDB; 1AR2; X-ray; @=1-107.		
DR	PDB; 1BW; X-ray; A/B=1-107.		
DR	PDB; 1REI; X-ray; A/B=1-107.		
DR	GO; GO:0005576; C:extracellular; NAS.		
DR	GO; GO:0003823; F:antigen binding; NAS.		
DR	GO; GO:0006955; P:immune response; NAS.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF00047; ig; 1.		
DR	SMART; SM00406; IGV; 1..		
DR	PROSITE; PS50835; IG_LIKE; 1.		
KW	3D-structure; Bence-Jones protein; Direct protein sequencing;		
KW	Immunoglobulin V region.		
FT	DOMAIN 1 23		
FT	DOMAIN 24 34		
FT	DOMAIN 35 49		
FT	DOMAIN 50 56		
FT	DOMAIN 57 88		
FT	DOMAIN 89 97		
FT	DOMAIN 98 107		
FT	DISULFID 23 88		
FT	STRAND 4 7		
FT	STRAND 10 13		
FT	TURN 15 16		
FT	STRAND 19 25		
FT	TURN 30 31		
FT	STRAND 33 38		
FT	TURN 40 41		
FT	STRAND 45 49		
FT	TURN 50 52		
FT	STRAND 53 54		
FT	TURN 56 57		
FT	TURN 60 61		
FT	STRAND 62 67		
FT	TURN 68 69		
FT	STRAND 70 75		



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FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match
Best Local Similarity 69.9%; Score 400; DB 1; Length 108;
Matches 76; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy 1 DIQMTQASSLPASLGRVTITSCASQDISNYLWYQOKPDGTVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQSSLSASVGDRTITCOASQDISNYLWYQOKPKAPKLLIYDASNLTCVPS 60
Qy 61 RFGSGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKTLEIKR 108
Db 61 RFGSGSGTDFTTISLQPEDVATYVCQYDNLPLTFFGGTKVDFKR 108

RESULT 13
KVLP_HUMAN STANDARD; PRT; 108 AA.
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Cum.)";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA Steimetz-Kayne M., Suter L., Watanabe S.;
RL (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New
RL York (1969).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (1,2)
marker.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91638; KIHURY.
DR HSSP; P01607; 1BWW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match
Best Local Similarity 69.8%; Score 399; DB 1; Length 108;
Matches 75; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Qy 1 DIQMTQASSLPASLGRVTITSCASQDISNYLWYQOKPDGTVKLLIFYSSNLHSGVPS 60
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Db 1 DIQMTQSSLSASVGDRTITCOASQDISIFLNWYQOKPGKAPKLLIYDASKLEAGVPS 60
Qy 61 RFGSGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKTLEIKR 108
Db 61 RFGSGSGTDFTTISLQPEDVATYVCQYDNLPLTFFGGTKVDFKR 108

RESULT 14
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cln.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; 1BWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 108 108
FT NON_TER 1
SQ SEQUENCE 108 AA; 11633 MW; B7BDC3E41FCCA37 CRC64;

Query Match
Best Local Similarity 69.2%; Score 396; DB 2; Length 108;
Matches 76; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy 1 DIQMTQASSLPASLGRVTITSCASQDISNYLWYQOKPDGTVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQSSLSASVGDRTITCOASQDISNYLWYQOKPGKAPKLLIYDASKLEAGVPS 60
Qy 61 RFGSGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGKTLEIKR 108
Db 61 RFGSGSGTDFTTISLQPEDVATYVCQYDNLPLTFFGGTKVDFKR 108

RESULT 15
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes.";

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RL J. Immunol. 161:2020-2031 (1998).
DR EMBL; U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSP; P01607; LBWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;

Query Match          69.0%; Score 394.5; DB 2; Length 107;
Best Local Similarity 72.5%; Pred. No. 1.9e-32;
Matches 79; Conservative 13; Mismatches 14; Indels 3; Gaps 2;

Qy 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
   |||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
Db 1 DIQMTQSPSSLASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
   |||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:

Qy 61 RPSGGSGGTDYSLTISNLEPEDIATYFCHQ-YSKLPWTFGGGTKLEIKR 108
   |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 61 RPSGGSGGTDFTLTISLQPEDFATYCCQSYSTL--TFGGGTKVEIKR 107
   |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
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Search completed: August 1, 2005, 09:17:10  
Job time : 28.0249 secs

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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:10 ; Search time 175.288 Seconds  
(without alignments)  
1284.140 Million cell updates/sec

Title: US-10-089-500-57

Perfect score: 3071

Sequence: 1 EVTLVESGGDFVKPGSLKV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3071	100.0	582	4 AAB81991	Aab81991 Ganglios
2	3076	98.5	582	4 AAB81987	Aab81987 Ganglios
3	2759.5	89.9	583	4 AAB83156	Aab83156 Ganglios
4	2744.5	89.4	579	6 AAE33444	Aae33444 KS antibo
5	2738.5	89.2	579	6 AAO30910	Aao30910 di-KS-ala
6	2731.5	88.9	581	4 AAB81972	Aab81972 Ganglios
7	2715.5	88.4	575	8 ADP42961	Adp42961 Humanised
8	2592	84.4	580	6 AAO30915	Aao30915 di-NHS76
9	2560	83.4	580	6 AAO30913	Ado30913 di-NHS76
10	2234	72.7	468	8 ADQ07413	Adq07413 Mature CB
11	2234	72.7	468	8 ADQ12196	Adq12196 CBE11 pen
12	2218.5	72.2	449	5 AAO18400	Aao18400 Mature hu
13	2218.5	72.2	697	8 ADQ07403	Adq07403 hCBE11/hb
14	2218.5	72.2	697	8 ADQ12180	Adq12180 Heavy cha
15	2218.5	72.2	701	8 ADQ07409	Adq07409 hCBE11 mo
16	2218.5	72.2	701	8 ADQ12186	Adq12186 Heavy cha
17	2216	72.2	713	8 ADN97491	Adn97491 Artificia
18	2216	72.2	713	8 ADN97489	Adn97489 Artificia
19	2209.5	71.9	475	7 ADM47075	Adm47075 Mouse ant
20	2205	71.8	477	2 AAR47453	Aar47453 chiT84.12
21	2203.5	71.8	471	8 ADM72029	Adm72029 Chimeric
22	2202	71.7	449	8 ADR23346	Adr23346 Human CD7
23	2201.5	71.7	447	6 AAE33522	Aae33522 Human AOC
24	2200.5	71.7	444	6 AAE35327	Aae35327 Humanised
25	2200.5	71.7	444	6 AAE34876	Aae34876 BIWA4/8 a

Adl15443	Humanised
Ado00851	Humanised
Aao31101	Human A2-
Aae33523	Human AOC
Adh34587	023 heavy
Abp58273	Humanised
Abp58275	Humanised
Aae33524	Human AOC
Adm72025	Chimeric
Adh34584	008 heavy
Adf11425	2D8 anti
Adp58494	Humanised
Aay68810	A rat hea
Aao14065	Heavy cha
Abu08017	Human mon
Adf65775	Human mon
Adj92515	Human SOJ
Adr39847	Hu266 N56
Abp39843	Hu266 N56
Abp39465	Humanised
Abu08311	Humanised
Abb80109	Heavy cha
Ades4066	Humanised
Adn61714	Humanised
Aau07745	Humanised
Abp39844	Hu266 N56
Abp39848	Hu266 N56
Aau14288	Human nov
Aar24812	Sequence
Adri0018	Human pro
Adf11421	2E11 anti
Adr23344	Human CD7
Adr23352	Human CD7
Adr23354	Human CD7
Adh34586	021 heavy
Aae12715	Human rec
Abu58807	Mucin 1 (
Adr2764	Human mon
Abu08320	Humanised
Abp39793	Humanised
Abp58013	Deglycosy
Ades4075	Humanised
Adf11433	16E1 anti
Adr09218	Human pro
Aar20057	Heavy cha
Adf11417	22B3 anti
Adf11429	18B2 anti
Adf11437	9H7 anti-
Adh34585	0011 heav
Aar42066	Human ant
Adma1561	Anti-inte
Aap60351	Chimeric
Aap70547	Sequence
Adm05955	Human pro
Aay29458	Recombina
Aay77766	Humanised
Abu13799	Humanised
Abu59512	Humanised
Aae33094	Protein #
Adm41555	Anti-inte
Adp79584	2H7.v16 H
Adr10009	Human pro
Adr19327	Chimeric
Adr19328	Chimeric
Aaw69316	Anti-IL-8
Adr66914	Human pro
Adr66016	Human pro
Abg78151	Human Fv
Abg91842	Human ant
Adq66840	Novel hum
Adf11670	anti-CD11

99 2135 69.5 461 2 AAR42162 Anti-HIV-  
100 2133.5 69.5 444 3 AAY32263 Humanised

ALIGNMENTS

RESULT 1  
AAB81991  
ID AAB81991 standard; protein; 582 AA.

AC AAB81991;  
DT 03-JUL-2001 (first entry)  
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
OS Synthetic.  
PN WO200123432-A1.  
PD 05-APR-2001.  
PF 29-SEP-2000; 2000WO-JP006774.  
PR 30-SEP-1999; 99JP-00278291.  
PR 06-APR-2000; 2000JP-00105088.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX Hanai N, Shitara K, Nakamura K, Niwa R;  
XX WPI; 2001-266143/27.  
XX New human type complementation-determining region-transplanted antibody,  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX Claim 39; Page 175-179; 183pp; Japanese.  
XX The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumors, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX  
XX Sequence 582 AA;

Query Match 100.0%; Score 3071; DB 4; Length 582;  
Best Local Similarity 100.0%; Pred. No. 4.6e-149;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EVTLVESGDFVKPGSLKVSAAAGFAPSHYAMSWVRQTPAKRLEWYAYISSGSGTYY 60  
DB 1 EVTLVESGDFVKPGSLKVSAAAGFAPSHYAMSWVRQTPAKRLEWYAYISSGSGTYY 60  
QY 61 SDSVKGRTISRDNANTLYLQWRSLSRSDSAMYFCTRVKLGTYVFDSWGQGTTLTVSSA 120  
DB 61 SDSVKGRTISRDNANTLYLQWRSLSRSDSAMYFCTRVKLGTYVFDSWGQGTTLTVSSA 120  
QY 121 STKGVSFFPLAPSSKTSSTGTAALGCLVKDYFPEPVTVSNWNSGALTSVGHTPPAVLQSSG 180  
DB 121 STKGVSFFPLAPSSKTSSTGTAALGCLVKDYFPEPVTVSNWNSGALTSVGHTPPAVLQSSG 180  
QY 181 LYSLSVTVTPSSSLGTQYIICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPELLGGP 240  
DB 181 LYSLSVTVTPSSSLGTQYIICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPELLGGP 240  
QY 241 SVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300

DB 241 SVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300  
QY 301 TYRVVSULTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360  
DB 301 TYRVVSULTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360  
QY 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQ 420  
DB 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQ 420  
QY 421 QGNVFSCSVMEALHNHYTQKSLSLSPGKAPTSSSTKTKTQLQLEHLLDQLQMILGINNY 480  
DB 421 QGNVFSCSVMEALHNHYTQKSLSLSPGKAPTSSSTKTKTQLQLEHLLDQLQMILGINNY 480  
QY 481 KNPKLTRMLTFKFMYPKATLKHQLCLEBELKPLEEVNLNAQSNFHLRPRDLISINV 540  
DB 481 KNPKLTRMLTFKFMYPKATLKHQLCLEBELKPLEEVNLNAQSNFHLRPRDLISINV 540  
QY 541 IVLELKGSETTFMCEYADETATIVFEFLNRWITFCQSIISTLT 582  
DB 541 IVLELKGSETTFMCEYADETATIVFEFLNRWITFCQSIISTLT 582

RESULT 2

AAB81987  
ID AAB81987 standard; protein; 582 AA.  
XX  
AC AAB81987;  
DT 03-JUL-2001 (first entry)  
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
OS Synthetic.  
XX WO200123432-A1.  
PN 05-APR-2001.  
PD 29-SEP-2000; 2000WO-JP006774.  
PF 30-SEP-1999; 99JP-00278291.  
PR 06-APR-2000; 2000JP-00105088.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX Hanai N, Shitara K, Nakamura K, Niwa R;  
XX WPI; 2001-266143/27.  
XX New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX Claim 41; Page 168-172; 183pp; Japanese.  
XX The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumors, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX  
XX Sequence 582 AA;

Query Match 98.5%; Score 3026; DB 4; Length 582;  
Best Local Similarity 98.3%; Pred. No. 9.1e-147;  
Matches 572; Conservative 5; Mismatches 5; Indels 0; Gaps 0;



Qy 1 EVTLVESGGDFVKPGSLKVSACASGAFSHYAMSWROTAPAKLEWAVISSGGSTYY 60  
 Db 1 EVQLVESGGDFVQPGSLRVSCASGAFSHYAMSWROAPGKLEWAVISSGGSTYY 60  
 Qy 61 SDSVKGRFTTISRDNAKNTLYLQMRSLRSDSAMYFCFTRVKLGTYYPDSWGGTLLTVSSA 120  
 Db 61 SDSVKGRFTTISRDNAKNTLYLQMRSLRSDSAMYFCFTRVKLGTYYPDSWGGTLLTVSSA 120  
 Qy 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180  
 Db 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180  
 Qy 181 LYSLSVSVTVPSSSLGQTQYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELLGGP 240  
 Db 181 LYSLSVSVTVPSSSLGQTQYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELLGGP 240  
 Qy 241 SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS 300  
 Db 241 SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS 300  
 Qy 301 TYRVSVSLTVLHODWLNKGEYKCKVSNKALPAIEKTIISKAGQPREPOVYITLPPSRDEL 360  
 Db 301 TYRVSVSLTVLHODWLNKGEYKCKVSNKALPAIEKTIISKAGQPREPOVYITLPPSRDEL 360  
 Qy 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSKLTVDKSRWQ 420  
 Db 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSKLTVDKSRWQ 420  
 Qy 421 QGNVFSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKTKTQLQLEHLLLDLQMLINGINNY 480  
 Db 421 QGNVFSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKTKTQLQLEHLLLDLQMLINGINNY 480  
 Qy 481 KNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVNLAQSKNPHLRPRDLISINIV 540  
 Db 481 KNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVNLAQSKNPHLRPRDLISINIV 540  
 Qy 541 IVLELKGSETTFMCEYADETATVEFLNRWITFCQSIISTLT 582  
 Db 541 IVLELKGSETTFMCEYADETATVEFLNRWITFCQSIISTLT 582

RESULT 3

AAE33444  
 ID AAE33444 standard; protein; 579 AA.  
 AC AAE33444;  
 DT 02-JUL-2001 (first entry)  
 DE Ganglioside GM2 antibody-related protein #1.  
 KW Ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer.  
 OS Unidentified.

XX WO200123431-A1.

XX 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006775.

XX 30-SEP-1999; 99JP-00278292.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

XX Hanai N, Nakamura K, Niwa R;

XX WPI; 2001-266142/27.

XX Monoclonal antibodies against ganglioside GM2 combined with drugs,  
 PT radioisotopes or proteins for treatment and diagnosis of cancer.

XX Claim 43; Page 61-65; 80pp; Japanese.

XX

The present invention relates to derivatives of an antibody against  
 CC ganglioside GM2. The antibody may be a monoclonal antibody or its  
 CC fragments. The antibody is combined with a radioactive isotope, protein  
 CC or small drug in the treatment and diagnosis of cancer

Qy Sequence 583 AA;

Query Match 89.9%; Score 2759.5; DB 4; Length 583;

Best Local Similarity 89.4%; Pred. No. 3.8e-133;

Matches 523; Conservative 21; Mismatches 36; Indels 5; Gaps 2;

Qy 1 EVTLVESGGDFVKPGSLKVSACASGAFSHYAMSWROTAPAKLEWAVISSGGSTYY 60

Db 1 EVQLVESGGDFVQPGSLRVSCASGAFSHYAMSWROAPGKLEWAVISSGGSTYY 60

Qy 61 SDSVKGRFTTISRDNAKNTLYLQMRSLRSDSAMYFCFTRVKLGTYYPDSWGGTLLTV 117

Db 61 NQKFKSKVTITVDITSTSTAYMELSLRSEDATVYIC--ATYGHYYGYMFAYWGGTLLTV 118

Qy 118 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 177

Db 119 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 178

Qy 178 SSGLYSLSSVTVPSSSLGQTQYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELL 237

Db 179 SSGLYSLSSVTVPSSSLGQTQYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELL 238

Qy 238 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 297

Db 239 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 298

Qy 298 YNSTYRVSVSLTVLHODWLNKGEYKCKVSNKALPAIEKTIISKAGQPREPOVYITLPPSR 357

Db 299 YNSTYRVSVSLTVLHODWLNKGEYKCKVSNKALPAIEKTIISKAGQPREPOVYITLPPSR 358

Qy 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSKLTVDKS 417

Db 359 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSKLTVDKS 418

Qy 418 RWQGNVFSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKTKTQLQLEHLLLDLQMLINGI 477

Db 419 RWQGNVFSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKTKTQLQLEHLLLDLQMLINGI 478

Qy 478 NNYKNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVNLAQSKNPHLRPRDLISN 537

Db 479 NNYKNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVNLAQSKNPHLRPRDLISN 538

Qy 538 INVIVLELKGSETTFMCEYADETATVEFLNRWITFCQSIISTLT 582

Db 539 INVIVLELKGSETTFMCEYADETATVEFLNRWITFCQSIISTLT 583

RESULT 4

AAE33444

ID AAE33444 standard; protein; 579 AA.

XX AAE33444;  
 AC AAE33444;

DT 02-APR-2003 (first entry)

DE KS antibody heavy chain-interleukin 2 (IL-2) fusion protein.

DE Immunoglobulin; diagnosis; epithelial cell adhesion molecule; EPCAM;  
 KW cancer; gene therapy; interleukin-2; IL2; fusion protein.

XX Unidentified.

XX WO200290566-A2.

XX 14-NOV-2002.

XX 03-MAY-2002; 2002WO-US013844.

PF

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XX 03-MAY-2001; 2001US-028564P.
PR (LEXI-) LEXIGEN PHARM CORP.
XX Gillies SD, Lo K, Qian X;
XX WPI; 2003-111985/10.
DR N-P5DB; AAD51139.
XX New recombinant anti-EpCAM antibody having an amino acid sequence
PT defining an immunoglobulin light or heavy chain framework region, useful
PT for the diagnosis, prognosis and treatment of cancer.
XX Disclosure; Page 80-82; 82pp; English.
XX The present invention relates to novel recombinant anti-EpCAM (human
CC epithelial cell adhesion molecule) antibodies comprising an amino acid
CC sequence defining an immunoglobulin light or heavy chain framework
CC region. Sequences of the present invention are useful for the diagnosis,
CC prognosis and treatment of cancer. They are also used in gene therapy.
CC The present sequence is KS antibody heavy chain-interleukin 2 (IL-2)
CC fusion protein. This sequence is used to illustrate the method of the
XX invention
XX Sequence 579 AA;
XX
XX Query Match 89.4%; Score 2744.5; DB 6; Length 579;
XX Best Local Similarity 88.5%; Pred. No. 2.2e-132;
XX Matches 516; Conservative 31; Mismatches 31; Indels 5; Gaps 2;
QY 1 EVTLVESGDFVKPGSLKVSAAAGFAPSHYAMSWVRQTAPKRLIEWAYISSGSGSTYY 60
DB 1 QIQLVQSGAEVKKPGETVKISKASGYTFNTYGMNVRQTPGKGLKMGWINTYTGPTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTR-VKLGTYTFDSWGGTTLTVSS 119
DB 61 ADDFKGRFAFSLTSTAFQINNLRSEDRTATYFCVRFISKGDY----WGQGSVTYSS 116
QY 120 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 179
DB 117 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 176
QY 180 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKRVPEKSCDKTHTCPPCPAPELLGG 239
DB 177 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKRVPEKSCDKTHTCPPCPAPELLGG 236
QY 240 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 299
DB 237 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 296
QY 300 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
DB 297 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 356
QY 360 LTRNQVSLTCLVKGPYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 419
DB 357 MTKNQVSLTCLVKGPYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 416
QY 420 QGQNVFSCSVMEALHNYTKQSLSLSPGKAPTSSSTTKTQLQLRHLLDLQMLINGNN 479
DB 417 QGQNVFSCSVMEALHNYTKQSLSLSPGKAPTSSSTTKTQLQLRHLLDLQMLINGNN 476
QY 480 YKNPKLTRMLTFKPYMPKKATELKHQLCEEELKPLEEVLNLAQSKNPHLRPRDLISIN 539
DB 477 YKNPKLTRMLTFKPYMPKKATELKHQLCEEELKPLEEVLNLAQSKNPHLRPRDLISIN 536
QY 540 VIVLELKGSETTFMCEYADETATIEVPLNRWITFCQSIISTLT 582
DB 537 VIVLELKGSETTFMCEYADETATIEVPLNRWITFCQSIISTLT 579
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AAO30910
ID AAO30910 standard; protein; 579 AA.
XX
XX AAO30910;
XX
XX 22-SEP-2003 (first entry)
XX
XX dI-KS-ala-IL2 (D20T) variant protein.
XX
XX Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
XX gene therapy; immunoglobulin; Ig; fusion protein; human.
XX
XX Homo sapiens.
XX Unidentified.
XX Chimeric.
XX
XX WO2003048334-A2.
XX
XX 12-JUN-2003.
XX
XX 04-DEC-2002; 2002WO-US038780.
XX
XX 04-DEC-2001; 2001US-0337113P.
XX
XX 12-APR-2002; 2002US-0371966P.
XX
XX (EMDL-) EMD LEXIGEN RES CENT CORP.
XX
XX Gillies SD;
XX
XX WPI; 2003-513757/48.
XX
XX New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
XX moiety, useful for preparing a composition for treating cancer, viral
XX infections or immune disorders.
XX
XX Example 10; Page 60-63; 71pp; English.
XX
XX The invention relates to cytokine fusion proteins with increased
XX therapeutic index and methods for increasing the therapeutic index of
XX such fusion proteins. The fusion protein comprises a non-interleukin-2
XX (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a
XX composition for treating cancer, viral infections or immune disorders.
XX The fusion protein is also used in gene therapy. The present sequence is
XX dI-KS-ala-IL2 (D20T) variant protein comprising di-KS heavy chain fused
XX to human IL-2 (D20T) variant protein. This sequence is used to illustrate
XX the method of the invention
XX
XX Sequence 579 AA;
XX
XX Query Match 89.2%; Score 2738.5; DB 6; Length 579;
XX Best Local Similarity 88.3%; Pred. No. 4.4e-132;
XX Matches 515; Conservative 30; Mismatches 33; Indels 5; Gaps 2;
QY 1 EVTLVESGDFVKPGSLKVSAAAGFAPSHYAMSWVRQTAPKRLIEWAYISSGSGSTYY 60
DB 1 QIQLVQSGPELKKPGSSVKISKASGYTFNTYGMNVRQAPGKGLKMGWINTYTGPTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTR-VKLGTYTFDSWGGTTLTVSS 119
DB 61 ADDFKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTR-VKLGTYTFDSWGGTTLTVSS 116
QY 120 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 179
DB 117 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 176
QY 180 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKRVPEKSCDKTHTCPPCPAPELLGG 239
DB 177 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKRVPEKSCDKTHTCPPCPAPELLGG 236
QY 240 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 299
DB 237 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 296
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QY 300 STYRVSVLTCLVHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 359  
DB 297 STYRVSVLTCLVHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 356  
QY 360 LTKNOVSLTCLVKGFPSPDIKAVESNGQDENNYKTPPVLDSDGSFFLYSKLTVDKSRW 419  
DB 357 MTKNOVSLTCLVKGFPSPDIKAVESNGQDENNYKTPPVLDSDGSFFLYSKLTVDKSRW 416  
QY 420 QQGNVFCSCVMHEALHNHYTKQSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLNGINN 479  
DB 417 QQGNVFCSCVMHEALHNHYTKQSATATPGAAPTSSSTKKTQLQLEHLLLDLQMLNGINN 476  
QY 480 YKNPKLTRMLTFKPYMPKKATELKHLCLEELKPLEEVNLQAQKNFHLRPRDLISIN 539  
DB 477 YKNPKLTRMLTFKPYMPKKATELKHLCLEELKPLEEVNLQAQKNFHLRPRDLISIN 536  
QY 540 VIVLELKGSETTFMCEYADETATIVBFLNRWITFCOSIISTLT 582  
DB 537 VIVLELKGSETTFMCEYADETATIVBFLNRWITFCOSIISTLT 579

RESULT 6  
ID AAB81972 standard; protein; 581 AA.  
XX AAB81972;  
AC AC  
XX AC  
DT 03-JUL-2001 (first entry)  
XX 03-JUL-2001 (first entry)  
DE Ganglioside GD2 specific antibody related protein SEQ ID NO: 31.  
XX Ganglioside; GD2; complementation determining region; CDR; antibody;  
KW Ganglioside; GD2; complementation determining region; CDR; antibody;  
XX mouse; cancer.  
OS Synthetic.  
XX Synthetic.  
PN WO200123573-A1.  
XX WO200123573-A1.  
PD 05-APR-2001.  
XX 05-APR-2001.  
PF 29-SEP-2000; 2000NO-JP006773.  
XX 29-SEP-2000; 2000NO-JP006773.  
PR 30-SEP-1999; 99JP-00278290.  
XX 30-SEP-1999; 99JP-00278290.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX Hanai N, Shitara K, Nakamura K, Niwa R;  
DR WPI; 2001-266163/27.  
XX WPI; 2001-266163/27.  
XX Human type complementation-determining domain transplanted antibody and  
PT derivatives against ganglioside GD2, useful in diagnosis and therapy of  
PT e.g. tumors, has low antigenicity, little side effects but potent  
PT activity in cancer.  
XX activity in cancer.  
XX Example 3; Page 111-114; 123pp; Japanese.  
XX Example 3; Page 111-114; 123pp; Japanese.  
CC The present invention describes an antibody, which can react specifically  
CC with ganglioside GD2, and is transplanted with a human type  
CC complementation-determining domain (CDR), or its fragments. The antibody  
CC and its derivatives are useful in diagnosis and therapy of tumors,  
CC particularly cancer diagnosis. The present sequence is a protein used in  
CC the exemplification of the invention  
XX the exemplification of the invention  
SQ Sequence 581 AA;

Query Match 88.9%; Score 2731.5; DB 4; Length 581;  
Best Local Similarity 89.0%; Pred. No. 1e-131;  
Matches 518; Conservative 24; Mismatches 39; Indels 1; Gaps 1;  
QY 1 EYTLVESGDFVKPGGSLKVCASGAFASHVYMSWVROTPAKRLBWVAYISGGSGTY 60  
DB 1 QVQLQESGPGLVKPSQTLTITCTVSGFSLASYNIHVVRPPGKGLWLGVIWAGGS-TNY 59

QY 61 SDSVKGKRPITSDNAKNTLYLQWRSLSRSDSAMFYCTRVKLGTYTFYFDSWGQGTTLTVSSA 120  
DB 60 NSALMSRLTISKDNSKNQVFLKMSLTAADTAVYCYAKESDDYSWFAYMGQGLTVTVSSA 119  
QY 121 STKGSPVFLAPSSSKSTSGGTAALGCLVKDYPPETVTVSNWNGALTSVGHVTFPAVLQSSG 180  
DB 120 STKGSPVFLAPSSSKSTSGGTAALGCLVKDYPPETVTVSNWNGALTSVGHVTFPAVLQSSG 179  
QY 181 LYSLSGVTVTPSSSLGTQYICNVNHNKPSNTKVDKAVKPKSCDKHTCPCPAPELGGP 240  
DB 180 LYSLSGVTVTPSSSLGTQYICNVNHNKPSNTKVDKAVKPKSCDKHTCPCPAPELGGP 239  
QY 241 SVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNNAKTKPREEQYNS 300  
DB 240 SVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNNAKTKPREEQYNS 299  
QY 301 TYRVSVLTCLVHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360  
DB 300 TYRVSVLTCLVHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 359  
QY 361 TKNQVSLTCLVKGFPSPDIKAVESNGQDENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ 420  
DB 360 TKNQVSLTCLVKGFPSPDIKAVESNGQDENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ 419  
QY 421 QGNVFCSCVMHEALHNHYTKQSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLNGINN 480  
DB 420 QGNVFCSCVMHEALHNHYTKQSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLNGINN 479  
QY 481 KNPKLTRMLTFKPYMPKKATELKHLCLEELKPLEEVNLQAQKNFHLRPRDLISIN 540  
DB 480 KNPKLTRMLTFKPYMPKKATELKHLCLEELKPLEEVNLQAQKNFHLRPRDLISIN 539  
QY 541 IVELELKGSETTFMCEYADETATIVBFLNRWITFCOSIISTLT 582  
DB 540 IVELELKGSETTFMCEYADETATIVBFLNRWITFCOSIISTLT 581

RESULT 7  
ID ADP42961 standard; protein; 575 AA.  
XX ADP42961;  
AC ADP42961;  
XX ADP42961;  
DT 23-SEP-2004 (first entry)  
XX 23-SEP-2004 (first entry)  
DE Humanised immunoglobulin heavy chain-IL-2 fusion protein SEQ ID NO:6.  
XX Humanised immunoglobulin heavy chain-IL-2 fusion protein SEQ ID NO:6.  
KW immunoglobulin; variable region; antibody; GD2; cytostatic; gene therapy;  
KW cancer; cell surface glycoephipingolipid; IL-2.  
OS Synthetic.  
XX Synthetic.  
PN WO2004055056-A1.  
XX WO2004055056-A1.  
PD 01-JUL-2004.  
XX 01-JUL-2004.  
PF 16-DEC-2003; 2003WO-EP014295.  
XX 16-DEC-2003; 2003WO-EP014295.  
PR 17-DEC-2003; 2002US-0433945P.  
XX 17-DEC-2003; 2002US-0433945P.  
PA (MERE ) MERCK PATENT GMBH.  
XX (MERE ) MERCK PATENT GMBH.  
PI Gillies SD, Lo K;  
XX Gillies SD, Lo K;  
DR WPI; 2004-488049/46.  
XX WPI; 2004-488049/46.  
DR N-PSDB; ADP42959.  
XX N-PSDB; ADP42959.  
PT New modified m14.18 antibodies with reduced immunogenicity and that  
PT specifically bind the human cell surface glycoephipingolipid GD2, useful  
XX for treating cancer.  
PS Disclosure; SEQ ID NO 6; 51pp; English.





CC which upon administration to a subject results in supra-additive  
CC inhibition of a tumour. The lymphotoxin-beta receptor agents have  
CC cytostatic activity. Gene therapy may be used in the tumour inhibition  
CC method. The method is useful for inhibiting tumour volume or for treating  
CC cancer. The lymphotoxin-beta receptor agonist and the chemotherapeutic  
CC agent are useful for preparing a medicament for the treatment of cancer,  
CC which upon administration to a subject results in supra-additive  
CC inhibition of a tumour. This sequence represents the mature CBEL1  
CC pentameric heavy chain antibody construct for use in the tumour volume  
CC inhibition method of the invention.  
XX  
XX SQ Sequence 468 AA;

Query Match 72.7%; Score 2234; DB 8; Length 468;  
Best Local Similarity 93.6%; Pred. No. 2.2e-106;  
Matches 424; Conservative 6; Mismatches 21; Indels 2; Gaps 2;  
QY 1 EYTLVESGGDFVKPGGSLKVSAAAGFAFASHYAMSWVROTAPAKRLEWVAYISSGGSGTY 60  
DB 1 EVQLVESGGGLVKPGGSLKLSAASGFTFSDYMYWFRQTPEKRLWVATISDGGSYTY 60  
QY 61 SDSVKGRFTISRDNKNTLYLQMSRLSDEDSAMYFCTRVKLTG-YYFDSWGGTTLTVSS 119  
DB 61 PDSVKGRFTISRDNKNTLYLQMSRLKSDTAMYYCVREENGNFYFDYWGQTTVTVSS 120  
QY 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179  
DB 121 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 180  
QY 180 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 239  
DB 181 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 240  
QY 240 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 299  
DB 241 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 300  
QY 300 STYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQRPFPQVYTLPPSRDE 359  
DB 421 QQGNVFCSCVMHEALHNHYTQKSLSLSTGK-PT 452

RESULT 11  
ID ADO12196 standard; protein; 468 AA.

XX ADO12196;  
XX  
XX  
XX  
XX CBEL1 pentameric heavy chain antibody.  
XX lymphotoxin-beta receptor; LT- $\alpha$ gr-R; Cytostatic; cancer; tumour;  
KW huCBEL1; huBHA10.  
XX Synthetic.  
XX WO2004058191-A2.  
XX  
XX  
XX  
XX 15-JUL-2004.

XX 22-DEC-2003; 2003WO-US041393.  
XX  
XX 20-DEC-2002; 2002US-0435154P.

PA (BIOG-) BIOGEN IDEC MA INC.  
XX Garber E, Bailly V, Browning JL;  
XX WPI; 2004-525790/50.  
DR N-PSDB; ADO12195.  
XX  
XX New multivalent antibody constructs specific for the human lymphotoxin-  
PT beta receptor, useful for diagnosing or treating cancer or for inhibiting  
PT tumor volume.  
XX  
XX Disclosure; SEQ ID NO 18; 85pp; English.  
XX  
XX The present invention relates to a multivalent antibody comprising at  
CC least one antigen recognition site specific for a lymphotoxin-beta  
CC receptor (LT- $\alpha$ gr; -R) epitope. The antibody is useful for preparing a  
CC medicament for the treatment of cancer. The composition and method are  
CC used for diagnosing or treating cancer and for inhibiting tumour volume.  
CC The present sequence represents CBEL1 pentameric heavy chain antibody.  
XX  
XX SQ Sequence 468 AA;

Query Match 72.7%; Score 2234; DB 8; Length 468;  
Best Local Similarity 93.6%; Pred. No. 2.2e-106;  
Matches 424; Conservative 6; Mismatches 21; Indels 2; Gaps 2;  
QY 1 EYTLVESGGDFVKPGGSLKVSAAAGFAFASHYAMSWVROTAPAKRLEWVAYISSGGSGTY 60  
DB 1 EVQLVESGGGLVKPGGSLKLSAASGFTFSDYMYWFRQTPEKRLWVATISDGGSYTY 60  
QY 61 SDSVKGRFTISRDNKNTLYLQMSRLSDEDSAMYFCTRVKLTG-YYFDSWGGTTLTVSS 119  
DB 61 PDSVKGRFTISRDNKNTLYLQMSRLKSDTAMYYCVREENGNFYFDYWGQTTVTVSS 120  
QY 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179  
DB 121 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 180  
QY 180 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 239  
DB 181 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 240  
QY 240 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 299  
DB 241 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 300  
QY 300 STYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQRPFPQVYTLPPSRDE 359  
DB 301 STYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQRPFPQVYTLPPSRDE 360  
QY 360 LTKQVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKGRW 419  
DB 361 LTKQVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKGRW 420  
QY 420 QQGNVFCSCVMHEALHNHYTQKSLSLSPGKAPT 452  
DB 421 QQGNVFCSCVMHEALHNHYTQKSLSLSTGK-PT 452

RESULT 12  
ID AAO18400 standard; protein; 449 AA.

XX AAO18400;  
XX  
XX  
XX 11-OCT-2002 (first entry)  
XX  
XX Mature humanised murine CBEL1 heavy chain variable domain.  
DE Mouse; humanised antibody; lymphotoxin beta receptor; antibody; cancer;  
KW neoplasia; LT-beta-R; light chain; heavy chain; variable region.  
XX  
XX Mus sp.

OS	Synthetic.	AC	ADQ07403;
XX	WO200230986-A2.	XX	07-OCT-2004 (first entry)
XX	18-APR-2002.	XX	hCBEl1/hBHA10 bispecific-1 antibody construct mature heavy chain.
XX	12-OCT-2001; 2001WO-US032140.	XX	tumour volume; lymphotoxin-beta receptor; LT-beta-R; agonist; antibody;
XX	13-OCT-2000; 2000US-0240285P.	KW	chemotherapeutic; supra-additive; inhibition; cytostatic; gene therapy;
PR	13-MAR-2001; 2001US-0275289P.	KW	cancer; mature heavy chain; hCBEl1/hBHA10 bispecific-1.
PR	21-JUN-2001; 2001US-0299987P.	XX	Homo sapiens.
XX	(BIOJ ) BIOGEN INC.	OS	Synthetic.
XX	Garber E, Lyne P, Saldanha JW;	XX	WO2004058183-A2.
XX	WPI; 2002-583337/62.	PN	15-JUL-2004.
XX	New humanized anti-lymphotoxin-beta receptor antibody, useful for	XX	22-DEC-2003; 2003WO-US041243.
PT	treating or reducing the advancement, severity or effects of neoplasia,	XX	20-DEC-2002; 2002US-0435185P.
PT	particularly solid tumors (i.e. carcinomas) including colorectal cancer	PR	(BIOG-) BIOGEN IDEC MA INC.
PT	and breast cancer.	XX	Lepage D, Gill A;
XX	Example 5; Page 25-26; 41pp; English.	PI	WPI; 2004-525785/50.
XX	The present invention relates to humanised anti-lymphotoxin beta receptor	XX	N-PSDB; ADQ07402.
CC	(LT-beta-R) antibodies. These are derived from the murine LT-beta-R	DR	Inhibiting tumor volume comprising administering an amount of a
CC	binding antibody CBEl1 and can be used to treat neoplasia in humans. The	XX	lymphotoxin-beta receptor agonist or antibody and a chemotherapeutic
CC	present sequence is a humanised murine CBEl1 heavy chain variable region	PT	agent (e.g. gemcitabine or adriamycin).
XX	Sequence 449 AA;	XX	Disclosure; SEQ ID NO 2; 161pp; English.
XX	Query Match 72.2%; Score 2218.5; DB 5; Length 449;	XX	The invention relates to a novel method for inhibiting tumour volume. The
XX	Best Local Similarity 93.1%; Pred. No. 1.3e-105;	XX	method comprises administering an amount of a lymphotoxin-beta receptor
XX	Matches 418; Conservative 9; Mismatches 21; Indels 1; Gaps 1;	CC	(LT-beta-R) agonist or antibody and an amount of at least one
Qy	1 EVTLVESGGDFVKPGGSLKVCASGAFSHYAMSWRQTPAKRLEWVAYISSGGSTYY 60	CC	chemotherapeutic agent, where the administration of the LT-beta-R agonist
Db	1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSYIMYFWRQAPGKLEWVATISDGSVITY 60	CC	or antibody and the chemotherapeutic agent results in supra-additive
Qy	61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMFYCTRVLGCT-YVFDWGGQTTLVSS 119	CC	inhibition of the tumour. The invention further relates to: a
Db	61 PDSVKGRFTISRDNKNSLYLQWSSLRSEDATVYYCAREENGNYFYFDYWGQGTIVTVSS 120	CC	pharmaceutical composition comprising an amount of an LT-beta-R agonist
Qy	120 ASTKGPSVFPFLAPSSKTSSTGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179	CC	and at least one chemotherapeutic agent, and a pharmaceutical carrier,
Db	121 ASTKGPSVFPFLAPSSKTSSTGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 180	CC	which upon administration to a subject results in supra-additive
Qy	180 GLYSLSGVTVVPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCDKHTCTCPCPAPELLGG 239	CC	inhibition of a tumour. The lymphotoxin-beta receptor agents have
Db	181 GLYSLSGVTVVPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCDKHTCTCPCPAPELLGG 240	CC	cytostatic activity. Gene therapy may be used in the tumour inhibition
Qy	240 PSVFLPPPKDITLMSRTPEVTCVVDVSHDEPVEKFNWYDGVVEVHNAKTPRBEQYN 299	CC	cancer. The lymphotoxin-beta receptor agonist and the chemotherapeutic
Db	241 PSVFLPPPKDITLMSRTPEVTCVVDVSHDEPVEKFNWYDGVVEVHNAKTPRBEQYN 300	CC	agent are useful for preparing a medicament for the treatment of cancer,
Qy	300 STRVSVSLTVLHQDMLNGEYKCKVSNKALPAPIETKISKAGQPREPOVYTLPPSRDE 359	CC	which upon administration to a subject results in supra-additive
Db	301 STRVSVSLTVLHQDMLNGEYKCKVSNKALPAPIETKISKAGQPREPOVYTLPPSRDE 360	CC	inhibition of a tumour. This sequence represents the mature heavy chain
Qy	360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 419	CC	of the hCBEl1/hBHA10 bispecific-1 antibody construct for use in the
Db	361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 420	CC	tumour volume inhibition method of the invention.
Qy	420 QQGNVFSCSWHEALHNNHYTKSLSPG 448	XX	Sequence 697 AA;
Db	421 QQGNVFSCSWHEALHNNHYTKSLSPG 449	XX	Query Match 72.2%; Score 2218.5; DB 8; Length 697;
XX	RESULT 13	XX	Best Local Similarity 93.1%; Pred. No. 2e-105;
ADQ07403		XX	Matches 418; Conservative 9; Mismatches 21; Indels 1; Gaps 1;
ID	ADQ07403 standard; protein; 697 AA.	Qy	1 EVTLVESGGDFVKPGGSLKVCASGAFSHYAMSWRQTPAKRLEWVAYISSGGSTYY 60
XX		Db	1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSYIMYFWRQAPGKLEWVATISDGSVITY 60
		Qy	61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMFYCTRVLGCT-YVFDWGGQTTLVSS 119
		Db	61 PDSVKGRFTISRDNKNSLYLQWSSLRSEDATVYYCAREENGNYFYFDYWGQGTIVTVSS 120
		Qy	120 ASTKGPSVFPFLAPSSKTSSTGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179
		Db	121 ASTKGPSVFPFLAPSSKTSSTGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 180
		Qy	180 GLYSLSGVTVVPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCDKHTCTCPCPAPELLGG 239
		Db	181 GLYSLSGVTVVPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCDKHTCTCPCPAPELLGG 240
		Qy	240 PSVFLPPPKDITLMSRTPEVTCVVDVSHDEPVEKFNWYDGVVEVHNAKTPRBEQYN 299
		Db	241 PSVFLPPPKDITLMSRTPEVTCVVDVSHDEPVEKFNWYDGVVEVHNAKTPRBEQYN 300
		Qy	300 STRVSVSLTVLHQDMLNGEYKCKVSNKALPAPIETKISKAGQPREPOVYTLPPSRDE 359
		Db	301 STRVSVSLTVLHQDMLNGEYKCKVSNKALPAPIETKISKAGQPREPOVYTLPPSRDE 360
		Qy	360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 419
		Db	361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 420
		Qy	420 QQGNVFSCSWHEALHNNHYTKSLSPG 448
		Db	421 QQGNVFSCSWHEALHNNHYTKSLSPG 449
		XX	ADQ07403
		XX	ID ADQ07403 standard; protein; 697 AA.
		XX	XX



Db 181 GLYSLSVVTVSSSLGTQTYICNVNHNKPSNTKVDKVKPEKSCDKTHTCCPCAPPELLGG 240  
QY 240 PSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299  
Db 241 PSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300  
QY 300 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRGPQVYTLPPSRDE 359  
Db 301 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRGPQVYTLPPSRDE 360  
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419  
Db 361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 420  
QY 420 QQGNVFSCSVNHEALHNHYTQKSLSLSPG 448  
Db 421 QQGNVFSCSVNHEALHNHYTQKSLSLSPG 449

RESULT 14  
ADQ12180  
ID ADQ12180 standard; protein; 697 AA.  
XX AC ADQ12180;  
XX DT 07-OCT-2004 (first entry)  
XX DE Heavy chain of huCBEl1/huBHA10 Bispecific-1 antibody.  
XX KW lymphotoxin-beta receptor; LT- $\delta$ gr-R; Cytostatic; cancer; tumour;  
XX KW huCBEl1, huBHA10.  
XX OS Homo sapiens.  
XX PN WO2004058191-A2.  
XX PD 15-JUL-2004.  
XX PF 22-DEC-2003; 2003WO-US041393.  
XX PR 20-DEC-2002; 2002US-0435154P.  
XX PA (BIOG-) BIOGEN IDEC MA INC.  
XX PI Garber E, Bailly V, Browning JL;  
XX DR WPI; 2004-525790/50.  
XX DR N-PSDB; ADQ12179.  
XX PT New multivalent antibody constructs specific for the human lymphotoxin-  
PT beta receptor, useful for diagnosing or treating cancer or for inhibiting  
PT tumor volume.  
XX PS Claim 27; SEQ ID NO 2; 85pp; English.  
XX CC The present invention relates to a multivalent antibody comprising at  
CC least one antigen recognition site specific for a lymphotoxin-beta  
CC receptor (LT- $\delta$ gr;-R) epitope. The antibody is useful for preparing a  
CC medicament for the treatment of cancer. The composition and method are  
CC used for diagnosing or treating cancer and for inhibiting tumour volume.  
CC The present sequence represents mature heavy chain of huCBEl1/huBHA10  
CC Bispecific-1 antibody.  
XX SQ Sequence 697 AA;

Query Match 72.2%; Score 2218.5; DB 8; Length 697;  
Best Local Similarity 93.1%; Pred. No. 2e-105;  
Matches 418; Conservative 9; Mismatches 21; Indels 1; Gaps 1;

QY 1 EYTLVESGGDFVKPGGSLKVKSCAASGFAPSHYAMSVRQTPAKRLWVAYISSGSGSTYY 60  
Db 1 EYQLVESGGGLVKPGGSLRLSCAASGFTSDYMYMYFRQAPGKGLWVATISDGGSTYY 60

QY 61 SDSVKGRTTISRDNKNTLYLQMSLRSEDSAMYPFCTRVKLTG - YFDSWGGTTLTVSS 119  
Db 61 PDSVKGRTTISRDNKNSLYLQMSLRADTAAYICAREENGNFYFDYWGQGTTVTVSS 120  
QY 120 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVLDYFPEPVTVMNSGALTSGVHTFPAVLQSS 179  
Db 121 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVLDYFPEPVTVMNSGALTSGVHTFPAVLQSS 180  
QY 180 GLYSLSVVTVSSSLGTQTYICNVNHNKPSNTKVDKVKPEKSCDKTHTCCPCAPPELLGG 239  
Db 181 GLYSLSVVTVSSSLGTQTYICNVNHNKPSNTKVDKVKPEKSCDKTHTCCPCAPPELLGG 240  
QY 240 PSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299  
Db 241 PSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300  
QY 300 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRGPQVYTLPPSRDE 359  
Db 301 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRGPQVYTLPPSRDE 360  
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419  
Db 361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 420  
QY 420 QQGNVFSCSVNHEALHNHYTQKSLSLSPG 448  
Db 421 QQGNVFSCSVNHEALHNHYTQKSLSLSPG 449

RESULT 15  
ADQ07409  
ID ADQ07409 standard; protein; 701 AA.  
XX AC ADQ07409;  
XX DT 07-OCT-2004 (first entry)  
XX DE hCBEl1 monospecific-1 antibody construct mature heavy chain.  
XX KW tumour volume; lymphotoxin-beta receptor; LT-beta-R; agonist; antibody;  
KW chemotherapeutic; supra-additive; inhibition; cytostatic; gene therapy;  
KW cancer; mature heavy chain; hCBEl1 monospecific-1.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN WO2004058183-A2.  
XX PD 15-JUL-2004.  
XX PF 22-DEC-2003; 2003WO-US041243.  
XX PR 20-DEC-2002; 2002US-0435185P.  
XX PA (BIOG-) BIOGEN IDEC MA INC.  
XX PI Lepage D, Gill A;  
XX WPI; 2004-525785/50.  
XX DR N-PSDB; ADQ07408.  
XX PT Inhibiting tumor volume comprising administering an amount of a  
PT lymphotoxin-beta receptor agonist or antibody and a chemotherapeutic  
PT agent (e.g. gemcitabine or adriamycin).  
XX PS Disclosure; SEQ ID NO 8; 161pp; English.  
XX CC The invention relates to a novel method for inhibiting tumour volume. The  
CC method comprises administering an amount of a lymphotoxin-beta receptor  
CC (LT-beta-R) agonist or antibody and an amount of at least one  
CC chemotherapeutic agent, where the administration of the LT-beta-R agonist  
CC or antibody and the chemotherapeutic agent results in supra-additive  
CC inhibition of the tumour. The invention further relates to: a



pharmaceutical composition comprising an amount of an Lr-beta-R agonist and at least one chemotherapeutic agent, and a pharmaceutical carrier, which upon administration to a subject results in supra-additive inhibition of a tumour. The lymphotoxin-beta receptor agents have cytostatic activity. Gene therapy may be used in the tumour inhibition method. The method is useful for inhibiting tumour volume or for treating cancer. The lymphotoxin-beta receptor agonist and the chemotherapeutic agent are useful for preparing a medicament for the treatment of cancer, which upon administration to a subject results in supra-additive inhibition of a tumour. This sequence represents the mature heavy chain of the hCBEL1 monospecific-1 antibody construct for use in the tumour volume inhibition method of the invention.

CC	XX	SQ	Sequence 701 AA;
Query Match			
Best Local Similarity 72.2%; Score 2218.5; DB 8; Length 701;			
Matches 418; Conservative 9; Mismatches 21; Indels 1; Gaps 1;			
Qy	1	EVTLVESGGDFVPGGSLKVS	CAASGPAFSGHYAMSWRQTPAKRLEWVAYISSGGSGTYY 60
Db	1	EVQLVESGGGLVPRGGSRL	LSCAASGFTSDYYWYFRAFGKGLWVATISDGSYTY 60
Qy	61	SDSVKGRFTISRDAKNTLV	LQWRLSRSDSAMFYCTRVLGT-YYPDSWGQGTTLTVSS 119
Db	61	PDSVKGRFTISRDAKNTLV	LQWRLSRSDSAMFYCTRVLGT-YYPDSWGQGTTLTVSS 120
Qy	120	ASTKGPSVFPLAPSSKST	SGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 179
Db	121	ASTKGPSVFPLAPSSKST	SGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 180
Qy	180	GLYSLSVWTVPSSSLGTQ	TYICNVNHKPSNTKYDKKVPKSCDKHTCTCPPELGG 239
Db	181	GLYSLSVWTVPSSSLGTQ	TYICNVNHKPSNTKYDKKVPKSCDKHTCTCPPELGG 240
Qy	240	PSVFLPPPKDITLMISRT	PEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
Db	241	PSVFLPPPKDITLMISRT	PEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300
Qy	300	STYRVSVLTIVLHODWLN	GKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 359
Db	301	STYRVSVLTIVLHODWLN	GKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 360
Qy	360	LTKNQVSLTCLVKGFYPS	DIAVESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 419
Db	361	LTKNQVSLTCLVKGFYPS	DIAVESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 420
Qy	420	QQGNVFSCSVMHEALHNH	YTKSLSPG 448
Db	421	QQGNVFSCSVMHEALHNH	YTKSLSPG 449

Search completed: August 1, 2005, 09:10:17  
Job time : 177.288 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 1, 2005, 08:59:16 ; Search time 44.1842 Seconds  
(without alignments)  
983.287 Million cell updates/sec

Title: US-10-089-500-57

Perfect score:

Sequence: 1 EVTLVESGGDFVKPGGSLKV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Minimum DB seq length: 0
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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%  
Maximum Match 100%

Maximum Match 100%  
Listing first 100 summaries

# Introduction

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/prodata/1/iaa/5A\_COMB.per:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Query			DB	ID	Description			
	Score	Match	Length						
1	2153.5	70.1	459	1	US-08-157-101A-7	Sequence 7,	Appli		
2	2149.5	70.0	452	3	US-09-027-449-71	Sequence 71,	Appli		
3	2149.5	70.0	452	3	US-09-026-985-71	Sequence 71,	Appli		
4	2149.5	70.0	452	4	US-09-121-952A-71	Sequence 71,	Appli		
5	2149.5	70.0	452	4	US-09-234-340A-71	Sequence 71,	Appli		
6	2124	69.2	453	3	US-08-466-151-8	Sequence 8,	Appli		
7	2124	69.2	453	3	US-08-466-151B-8	Sequence 8,	Appli		
8	2124	69.2	453	4	US-09-802-096B-8	Sequence 8,	Appli		
9	2124	69.2	453	4	US-09-802-077-8	Sequence 8,	Appli		
10	2122	69.1	451	2	US-08-887-352B-14	Sequence 14,	Appli		
11	2122	69.1	451	2	US-08-887-352B-16	Sequence 16,	Appli		
12	2122	69.1	451	3	US-08-466-151-65	Sequence 65,	Appli		
13	2122	69.1	451	3	US-09-109-207C-14	Sequence 14,	Appli		
14	2122	69.1	451	3	US-09-109-207C-16	Sequence 16,	Appli		
15	2122	69.1	451	3	US-09-296-005-14	Sequence 14,	Appli		
16	2122	69.1	451	3	US-09-296-005-16	Sequence 16,	Appli		
17	2122	69.1	451	4	US-09-920-171-14	Sequence 14,	Appli		
18	2122	69.1	451	4	US-09-920-171-16	Sequence 16,	Appli		
19	2122	69.1	451	4	US-09-716-028-14	Sequence 14,	Appli		
20	2122	69.1	451	4	US-09-716-028-16	Sequence 16,	Appli		
21	2122	69.1	451	4	US-10-113-996-14	Sequence 14,	Appli		
22	2122	69.1	451	4	US-10-113-996-16	Sequence 16,	Appli		
23	2118	69.0	451	2	US-08-887-352B-18	Sequence 18,	Appli		
24	2118	69.0	451	3	US-09-109-207C-18	Sequence 18,	Appli		
25	2118	69.0	451	3	US-09-282-503-2	Sequence 2,	Appli		
26	2118	69.0	451	3	US-09-054-255-2	Sequence 2,	Appli		
27	2118	69.0	451	3	US-09-296-005-18	Sequence 18,	Appli		

## ALIGNMENTS

## RESULT 1

US-08-157-101A-7  
; Sequence 7, Application US/08157101A  
; Patent No. 5808032  
; GENERAL INFORMATION:  
; APPLICANT: KURIHARA, TATSUYA  
; APPLICANT: MATSUKURA, SHIGEKAZU  
; APPLICANT: TSURUOKA, NOBUO  
; APPLICANT: ARIMA, KENJI  
; APPLICANT: NISHIHARA, TATSURO  
; TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION  
; TITLE OF INVENTION: PLASMIDS THEREFOR  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/157,101A  
; FILING DATE: 05-APR-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: TITUS, MARLANA K  
; REGISTRATION NUMBER: 35843  
; REFERENCE/DOCKET NUMBER: 9437/204199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3711  
; TELEFAX: 202-822-0944  
; TELEFAX: 6714627 CUCH  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 459 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-157-101A-7

Query Match 70.1%; Score 2153.5; DB 1; Length 459;  
Best Local Similarity 89.8%; Pred. No. 1.4e-159;  
Matches 404; Conservative 20; Mismatches 25; Indels 1; Gaps 1;  
QY 1 EYTLVESGDFVKPGSLKVSAAAGFAFHYAMSWRQTPAKRLEWVAYISSGGSGTY 60  
DB 10 QVLVESGGVVPQGRSLRLSCAASGFTFSSNSMHWVRQAPGKLEWVAVILYDGNHKFY 69  
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSDSAMYFCTRVK-LGTYFFDSWGQGLTLTVSS 119  
DB 70 ADSVKGRFTISRDNKNTLYLQMSLRSDSAMYFCTRVK-LGTYFFDSWGQGLTLTVSS 129  
QY 120 ASTKGPSVPLAPSSKTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 179  
DB 130 ASTKGPSVPLAPSSKTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 189  
QY 180 GLYSLSVVTVSSSLGTQTYICNNHSPSNTKVDKVEPKSCDKTHTCPCPAPDELGG 239  
DB 190 GLYSLSVVTVSSSLGTQTYICNNHSPSNTKVDKVEPKSCDKTHTCPCPAPDELGG 249  
QY 240 PSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 299

DB 250 PSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 309  
QY 300 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISAKAGQPREPQVYITLPPSRDE 359  
DB 310 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISAKAGQPREPQVYITLPPSRDE 369  
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 419  
DB 370 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 429  
QY 420 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449  
DB 430 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 459

## RESULT 2

US-09-027-449-71  
; Sequence 71, Application US/09027449  
; Patent No. 6025158  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/027,449  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/074,330  
; FILING DATE: 22-Jan-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/038,664  
; FILING DATE: 21-Feb-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R3-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 452 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

US-09-027-449-71

Query Match 70.0%; Score 2149.5; DB 3; Length 452;  
Best Local Similarity 88.7%; Pred. No. 2.9e-159;  
Matches 401; Conservative 19; Mismatches 29; Indels 3; Gaps 1;  
QY 1 EYTLVESGDFVKPGSLKVSAAAGFAFHYAMSWRQTPAKRLEWVAYISSGGSGTY 60  
DB 1 EVQLVQSGGVLVQPGSLRLSCAASGYSFSSHYHWVRQAPGKLEWVGYIDPSNGETTY 60  
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSDSAMYFCTRVK-LGTYFFDSWGQGLTLTV 117  
DB 61 NQKFKGRFTLSRDNSKNTAYLQMSLRSDSAMYFCTRVK-LGTYFFDSWGQGLTLTV 120



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; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-121-952A-71

Query Match      70.0%; Score 2149.5; DB 4; Length 452;
Best Local Similarity 88.7%; Pred. No. 2.9e-159;
Matches 401; Conservative 19; Mismatches 29; Indels 3; Gaps 1;

QY 1 EVTLVESGGDFVKPGSLKVSAAAGFAPFASHYAMSWRQTPAKRLEWVAYISSGSGTY 60
DB 1 EVQLVQSGGGLVQPGSLRLSCAASGYFSFHHYHWRQAPGKGLEWGYIDPSNGETTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKL---GTYFDSNGQGTTLTV 117
DB 61 NQKFKGRFTLSRDNSKNTAYLQMSLRRAEDTAVYYCARGDYRYNGDWFDFVWGQGTTLTV 120
QY 118 SSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQ 177
DB 121 SSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQ 180
QY 178 SSGLYSLSSVTVPSSSLGTTQYICNVNHPKSNKVDKKVPEKSCDKTHTCPPCPAPELL 237
DB 181 SSGLYSLSSVTVPSSSLGTTQYICNVNHPKSNKVDKKVPEKSCDKTHTCPPCPAPELL 240
QY 238 GGPSVFLPPPKDPTLMISRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
DB 241 GGPSVFLPPPKDPTLMISRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300
QY 298 YNSTYRVVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
DB 301 YNSTYRVVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 417
DB 361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 420
QY 418 RWOQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
DB 421 RWOQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452

RESULT 5
US-09-234-340A-71
; Sequence 71, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,340A
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952
; FILING DATE: 24-Jul-1998
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-234-340A-71

Query Match      70.0%; Score 2149.5; DB 4; Length 452;
Best Local Similarity 88.7%; Pred. No. 2.9e-159;
Matches 401; Conservative 19; Mismatches 29; Indels 3; Gaps 1;

QY 1 EVTLVESGGDFVKPGSLKVSAAAGFAPFASHYAMSWRQTPAKRLEWVAYISSGSGTY 60
DB 1 EVQLVQSGGGLVQPGSLRLSCAASGYFSFHHYHWRQAPGKGLEWGYIDPSNGETTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMFYCTRVKL---GTYFDSNGQGTTLTV 117
DB 61 NQKFKGRFTLSRDNSKNTAYLQMSLRRAEDTAVYYCARGDYRYNGDWFDFVWGQGTTLTV 120
QY 118 SSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQ 177
DB 121 SSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQ 180
QY 178 SSGLYSLSSVTVPSSSLGTTQYICNVNHPKSNKVDKKVPEKSCDKTHTCPPCPAPELL 237
DB 181 SSGLYSLSSVTVPSSSLGTTQYICNVNHPKSNKVDKKVPEKSCDKTHTCPPCPAPELL 240
QY 238 GGPSVFLPPPKDPTLMISRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
DB 241 GGPSVFLPPPKDPTLMISRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300
QY 298 YNSTYRVVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
DB 301 YNSTYRVVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 417
DB 361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 420
QY 418 RWOQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
DB 421 RWOQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452

RESULT 6
US-08-466-151-8
; Sequence 8, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
```

CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,151  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/466163  
FILING DATE: 06-Jun-1995  
APPLICATION NUMBER: 08/405617  
FILING DATE: 15-MAR-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/185899  
FILING DATE: 26-JAN-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/879495  
FILING DATE: 07-MAY-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718P2C1D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 453 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-466-151-8

Query Match 69.2%; Score 2124; DB 3; Length 453;  
Best Local Similarity 88.8%; Pred. No. 2.8e-157;  
Matches 403; Conservative 21; Mismatches 24; Indels 6; Gaps 4;  
QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF--SHYAMSVVROTAPAKRLEWVAYISGGSGTY 59  
DB 1 EVQLVESGGGLVQPGGSLRLS CAVGSYISITSGYSWNIROAPKGLEWVASITYDGS-TN 59  
QY 60 YSDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVK--LGTYYFDSWGQGTTLTV 117  
DB 60 YADSVKGRFTISRDDSKNTFYLMNSLR AEDTAVYYCARGSHYFGHWHFAVMQGTTLTV 119  
QY 118 SSAST--KGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 175  
DB 120 SSASTKGKPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 179  
QY 176 LQSSGLYSLSVVTPSSSLGTQTYICNVNHPKSN TKVDKVPKSCDKTHTCPPCPAPE 235  
DB 180 LQSSGLYSLSVVTPSSSLGTQTYICNVNHPKSN TKVDKVPKSCDKTHTCPPCPAPE 239  
QY 236 LLGGPSVFLFPPPKD TLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 295  
DB 240 LLGGPSVFLFPPPKD TLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 299  
QY 296 EQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPI EKTISKAKGQPREPQVYTLPP 355  
DB 300 EQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPI EKTISKAKGQPREPQVYTLPP 359  
QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPVLDSDGSFFLYSKLTVD 415  
DB 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPVLDSDGSFFLYSKLTVD 419

QY 416 KSRWQOGNVFSCSVMH EALHNHYTQKSLSLSPGK 449  
DB 420 KSRWQOGNVFSCSVMH EALHNHYTQKSLSLSPGK 453  
RESULT 7  
US-08-466-163B-8  
; Sequence 8, Application US/08466163B  
; Patent No. 6329509  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; FILE REFERENCE: P0718P2C1D1  
; CURRENT APPLICATION NUMBER: US/08/466,163B  
; CURRENT FILING DATE: 1995-06-06  
; PRIORITY APPLICATION NUMBER: US 08/405,617  
; PRIORITY FILING DATE: 1995-03-15  
; PRIORITY APPLICATION NUMBER: US 08/185,899  
; PRIORITY FILING DATE: 1994-01-26  
; PRIORITY APPLICATION NUMBER: US 07/879,495  
; PRIORITY FILING DATE: 1992-05-07  
; PRIORITY APPLICATION NUMBER: US 07/744,768  
; PRIORITY FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 8  
; LENGTH: 453  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized mae11, version 1 heavy chain  
US-08-466-163B-8

Query Match 69.2%; Score 2124; DB 3; Length 453;  
Best Local Similarity 88.8%; Pred. No. 2.8e-157;  
Matches 403; Conservative 21; Mismatches 24; Indels 6; Gaps 4;  
QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAF--SHYAMSVVROTAPAKRLEWVAYISGGSGTY 59  
DB 1 EVQLVESGGGLVQPGGSLRLS CAVGSYISITSGYSWNIROAPKGLEWVASITYDGS-TN 59  
QY 60 YSDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVK--LGTYYFDSWGQGTTLTV 117  
DB 60 YADSVKGRFTISRDDSKNTFYLMNSLR AEDTAVYYCARGSHYFGHWHFAVMQGTTLTV 119  
QY 118 SSAST--KGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 175  
DB 120 SSASTKGKPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 179  
QY 176 LQSSGLYSLSVVTPSSSLGTQTYICNVNHPKSN TKVDKVPKSCDKTHTCPPCPAPE 235  
DB 180 LQSSGLYSLSVVTPSSSLGTQTYICNVNHPKSN TKVDKVPKSCDKTHTCPPCPAPE 239  
QY 236 LLGGPSVFLFPPPKD TLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 295  
DB 240 LLGGPSVFLFPPPKD TLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 299  
QY 296 EQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPI EKTISKAKGQPREPQVYTLPP 355  
DB 300 EQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPI EKTISKAKGQPREPQVYTLPP 359  
QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPVLDSDGSFFLYSKLTVD 415  
DB 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPVLDSDGSFFLYSKLTVD 419  
QY 416 KSRWQOGNVFSCSVMH EALHNHYTQKSLSLSPGK 449  
DB 420 KSRWQOGNVFSCSVMH EALHNHYTQKSLSLSPGK 453  
RESULT 8  
US-09-802-096-8  
; Sequence 8, Application US/09802096





ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA: US/08/887,352B  
APPLICATION NUMBER: US/08/887,352B  
FILING DATE: 03-Jul-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P1123  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 451 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-887-352B-14

Query Match 69.1%; Score 2122; DB 2; Length 451;  
Best Local Similarity 88.7%; Pred. No. 4e-157;  
Matches 401; Conservative 21; Mismatches 26; Indels 4; Gaps 3;

QY 1 EVTLVSGGDFVKGKSLKVCASGAF-SHYAMSVWRTQPAKLEWVAYISGGSGTY 59  
Db 1 EVQLVSGGGLVQPGSLRSCAVSGYSITSGYSWNIQAPGKLEWVASIYDGS-TN 59  
QY 60 YDSVKGRTISRDNKNTLYLQMSLRSEDSAMYFCTRVK--LGTYYFDSWGGTTLTV 117  
Db 60 YNPSVKGRTISRDDSKNTFYLMNSLRADTAVYICARSHYFGHHFAVWGQTLTV 119  
QY 118 SSASTKGPSVFLAPLAPSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQ 177  
Db 120 SSASTKGPSVFLAPLAPSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQ 179  
QY 178 SGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELL 237  
Db 180 SGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELL 239  
QY 238 GGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297  
Db 240 GGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299  
QY 298 YNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357  
Db 300 YNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359  
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKS 417  
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKS 419  
QY 418 RMOQGNVFCSCVMHEALHNYTKQSLSPGK 449  
Db 420 RMOQGNVFCSCVMHEALHNYTKQSLSPGK 451

RESULT 11  
US-08-887-352B-16  
Sequence 16, Application US/08887352B  
Patent No. 5994511  
GENERAL INFORMATION:  
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
TITLE OF INVENTION: Improving Polypeptides  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way

CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA: US/08/887,352B  
APPLICATION NUMBER: US/08/887,352B  
FILING DATE: 03-Jul-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P1123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 451 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-887-352B-16

Query Match 69.1%; Score 2122; DB 2; Length 451;  
Best Local Similarity 88.7%; Pred. No. 4e-157;  
Matches 401; Conservative 21; Mismatches 26; Indels 4; Gaps 3;

QY 1 EVTLVSGGDFVKGKSLKVCASGAF-SHYAMSVWRTQPAKLEWVAYISGGSGTY 59  
Db 1 EVQLVSGGGLVQPGSLRSCAVSGYSITSGYSWNIQAPGKLEWVASIYDGS-TN 59  
QY 60 YDSVKGRTISRDNKNTLYLQMSLRSEDSAMYFCTRVK--LGTYYFDSWGGTTLTV 117  
Db 60 YNPSVKGRTISRDDSKNTFYLMNSLRADTAVYICARSHYFGHHFAVWGQTLTV 119  
QY 118 SSASTKGPSVFLAPLAPSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQ 177  
Db 120 SSASTKGPSVFLAPLAPSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQ 179  
QY 178 SGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELL 237  
Db 180 SGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELL 239  
QY 238 GGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297  
Db 240 GGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299  
QY 298 YNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357  
Db 300 YNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359  
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKS 417  
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKS 419  
QY 418 RMOQGNVFCSCVMHEALHNYTKQSLSPGK 449  
Db 420 RMOQGNVFCSCVMHEALHNYTKQSLSPGK 451

RESULT 12  
US-08-466-151-65  
Sequence 65, Application US/08466151  
Patent No. 6037453  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 65

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,151  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/466163  
; FILING DATE: 06-Jun-1995  
; APPLICATION NUMBER: 08/405617  
; FILING DATE: 15-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/185899  
; FILING DATE: 26-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/879495  
; FILING DATE: 07-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/744768  
; FILING DATE: 14-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P0718P2C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 451 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-08-466-151-65

Query Match 69.1%; Score 2122; DB 3; Length 451;  
Best Local Similarity 88.7%; Pred. No. 4e-157;  
Matches 401; Conservative 21; Mismatches 26; Indels 4; Gaps 3;  
QY 1 EVTLVESGGDFVKPGGSLKVS CAASGPAP-SHYAMSWVRQTPAKLEWVAYISSGSGCTY 59  
DB 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59  
QY 60 YSDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVK--LGTYVFDSWGQGTTLTV 117  
DB 60 YNPVKGRITISRDDSKNTFYLMNSLRAEDTAVYICARGSHYFGHMFHAVWGQGLTVTV 119  
QY 118 SSASTKGPSVFPPLAPSSKSTGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQ 177  
DB 120 SSASTKGPSVFPPLAPSSKSTGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQ 179  
QY 178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237  
DB 180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 239  
QY 238 GGPSVFLPPPKPKDMLSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297  
DB 240 GGPSVFLPPPKPKDMLSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299  
QY 298 YNSTYRVVSVLTVLHQQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 357  
DB 300 YNSTYRVVSVLTVLHQQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 359  
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 417

RESULT 14  
US-09-109-207C-16  
; Sequence 16, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:

Db 360 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 419  
QY 418 RWQQGNVFSCSVMEALHNHYTQKSLSLSPGK 449  
Db 420 RWQQGNVFSCSVMEALHNHYTQKSLSLSPGK 451  
RESULT 13  
US-09-109-207C-14  
; Sequence 14, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; CURRENT FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 14  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial  
; LOCATION: 1-451  
; OTHER INFORMATION: Heavy chain sequence derived from MAE11  
; US-09-109-207C-14

Query Match 69.1%; Score 2122; DB 3; Length 451;  
Best Local Similarity 88.7%; Pred. No. 4e-157;  
Matches 401; Conservative 21; Mismatches 26; Indels 4; Gaps 3;  
QY 1 EVTLVESGGDFVKPGGSLKVS CAASGPAP-SHYAMSWVRQTPAKLEWVAYISSGSGCTY 59  
DB 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59  
QY 60 YSDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVK--LGTYVFDSWGQGTTLTV 117  
DB 60 YNPVKGRITISRDDSKNTFYLMNSLRAEDTAVYICARGSHYFGHMFHAVWGQGLTVTV 119  
QY 118 SSASTKGPSVFPPLAPSSKSTGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQ 177  
DB 120 SSASTKGPSVFPPLAPSSKSTGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQ 179  
QY 178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237  
DB 180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 239  
QY 238 GGPSVFLPPPKPKDMLSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297  
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DB 300 YNSTYRVVSVLTVLHQQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 359  
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 417  
Db 360 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 419  
QY 418 RWQQGNVFSCSVMEALHNHYTQKSLSLSPGK 449  
Db 420 RWQQGNVFSCSVMEALHNHYTQKSLSLSPGK 451  
RESULT 14  
US-09-109-207C-16  
; Sequence 16, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
FILE REFERENCE: P1123R1  
CURRENT APPLICATION NUMBER: US/09/109,207C  
CURRENT FILING DATE: 1998-06-30  
PRIOR APPLICATION NUMBER: US 60/051,554  
PRIOR FILING DATE: 1997-07-03  
NUMBER OF SEQ ID NOS: 44  
SEQ ID NO 16  
LENGTH: 451  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
NAME/KEY: Artificial  
LOCATION: 1-451  
OTHER INFORMATION: Heavy chain sequence derived from MAE11  
US-09-109-207C-16

Query Match 69.1%; Score 2122; DB 3; Length 451;  
Best Local Similarity 88.7%; Pred. No. 4e-157;  
Matches 401; Conservative 21; Mismatches 26; Indels 4; Gaps 3;

Qy 1 EVTLVESGGDFVKPGGSLKVSACGAPF-SHYAMSHVROTAPAKRLWVAYISGGSGTY 59  
Db 1 EVOLVESGGGLVQPGGSLRLSCAVSYISITSGYSWNIROAPGKLEWVASITYDGS-TN 59  
Qy 60 YSDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVK--LGTYYFDSWGQGLTLTV 117  
Db 60 YNPSVKGRITISRDDSKNTFYLQMSLRADTAIVYICARGSHYFGHWHFAVWGQGLTLTV 119  
Qy 118 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVLQ 177  
Db 120 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVLQ 179  
Qy 178 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELL 237  
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELL 239  
Qy 238 GGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 297  
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Qy 298 YNSTYRWVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 357  
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Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKS 419  
Qy 418 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449  
Db 420 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 15  
US-09-296-005-14  
Sequence 14. Application US/09296005  
Patent No. 6290957  
GENERAL INFORMATION:  
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
FILE REFERENCE: P1123C1r  
CURRENT APPLICATION NUMBER: US/09/296,005  
CURRENT FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 08/887,352  
EARLIER FILING DATE: 1997-07-02  
NUMBER OF SEQ ID NOS: 26  
SEQ ID NO 14  
LENGTH: 451  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:

NAME/KEY: Artificial  
LOCATION: 1-451  
OTHER INFORMATION: Heavy chain sequence derived from MAE11  
US-09-296-005-14

Query Match 69.1%; Score 2122; DB 3; Length 451;  
Best Local Similarity 88.7%; Pred. No. 4e-157;  
Matches 401; Conservative 21; Mismatches 26; Indels 4; Gaps 3;

Qy 1 EVTLVESGGDFVKPGGSLKVSACGAPF-SHYAMSHVROTAPAKRLWVAYISGGSGTY 59  
Db 1 EVOLVESGGGLVQPGGSLRLSCAVSYISITSGYSWNIROAPGKLEWVASITYDGS-TN 59  
Qy 60 YSDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVK--LGTYYFDSWGQGLTLTV 117  
Db 60 YNPSVKGRITISRDDSKNTFYLQMSLRADTAIVYICARGSHYFGHWHFAVWGQGLTLTV 119  
Qy 118 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVLQ 177  
Db 120 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVLQ 179  
Qy 178 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELL 237  
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELL 239  
Qy 238 GGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 297  
Db 240 GGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 299  
Qy 298 YNSTYRWVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 357  
Db 300 YNSTYRWVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 359  
Qy 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKS 417  
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKS 419  
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Search completed: August 1, 2005, 09:20:56  
Job time : 45.1842 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 1, 2005, 09:02:01 ; Search time 153.558 Seconds  
(without alignments)  
1476.651 Million cell updates/sec

Title: US-10-089-500-57

Perfect score: 3071

Sequence: 1 EVTLVSGGDFVKPGSLKV.....IVEFLNRWTFQSIISTLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389508008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
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20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
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22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2744.5	89.4	579	14	US-10-138-727A-41
2	2738.5	89.2	579	14	US-10-310-719-32
3	2715.5	88.4	575	16	US-10-737-208A-6
4	2592	84.4	580	14	US-10-310-719-37
5	2560	83.4	580	14	US-10-310-719-35
6	2218.5	72.2	663	15	US-10-412-406-32
7	2218.5	72.2	4852	15	US-10-412-406-33
8	2216	72.2	713	16	US-10-679-620-64
9	2216	72.2	715	16	US-10-679-620-62
10	2205	71.8	464	17	US-10-938-353-102
11	2201.5	71.7	447	15	US-10-474-832-4
					Sequence 41, Appl
					Sequence 32, Appl
					Sequence 6, Appl
					Sequence 37, Appl
					Sequence 35, Appl
					Sequence 32, Appl
					Sequence 33, Appl
					Sequence 64, Appl
					Sequence 62, Appl
					Sequence 102, Appl
					Sequence 4, Appl

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Sequence 14, Appl  
Sequence 16, Appl  
Sequence 65, Appl  
Sequence 14, Appl  
Sequence 16, Appl

85 2122 69.1 451 16 US-10-813-483-4 Sequence 4, Appl  
86 2122 69.1 451 16 US-10-813-483-5 Sequence 5, Appl  
87 2122 69.1 451 16 US-10-791-619-14 Sequence 14, Appl  
88 2122 69.1 451 16 US-10-791-619-16 Sequence 16, Appl  
89 2122 69.1 451 17 US-10-714-000-2 Sequence 2, Appl  
90 2122 69.1 451 17 US-10-698-073-9 Sequence 9, Appl  
91 2122 69.1 451 17 US-10-968-237-65 Sequence 65, Appl  
92 2122 69.1 451 20 US-11-013-966-4 Sequence 4, Appl  
93 2122 69.1 451 20 US-11-013-966-5 Sequence 5, Appl  
94 2122 69.1 468 15 US-10-377-109-2 Sequence 2, Appl  
95 2122 69.1 476 14 US-10-020-786-11 Sequence 11, Appl  
96 2122 69.1 476 17 US-10-697-995-9 Sequence 9, Appl  
97 2122 69.1 667 16 US-10-764-428-7 Sequence 7, Appl  
98 2122 69.1 669 16 US-10-764-428-21 Sequence 21, Appl  
99 2121 69.1 472 15 US-10-108-260A-4295 Sequence 4295, Ap  
100 2120.5 69.0 447 16 US-10-379-392-118 Sequence 118, App

## ALIGNMENTS

## RESULT 1

US-10-138-727A-41  
; Sequence 41, Application US/10138727A  
; Publication No. US20030157054A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Qian, Susan  
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
; FILE REFERENCE: LEX-019  
; CURRENT APPLICATION NUMBER: US/10/138,727A  
; CURRENT FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: US 60/288,564  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 41  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: heavy chain-IL2  
US-10-138-727A-41

Query Match 89.4%; Score 2744.5; DB 14; Length 579;  
Best Local Similarity 88.5%; Pred. No. 1.2e-166;  
Matches 516; Conservative 31; Mismatches 31; Indels 5; Gaps 2;

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DB 1 QIQLVQSGAEVKKPGETVKIKSCASGYFTTNYGMNVRQTPGKGLKMWGINTYTGPTY 60  
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTR-VKLGTYVYFDSWGGTTLTVSS 119  
DB 61 ADDFKGRFAFSLTSTAFQINLRSEDATATYFCVRFISKGDY----WGQTSVTYSS 116  
QY 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 179  
DB 117 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 176  
QY 180 GLYSLSVVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 239  
DB 177 GLYSLSVVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 236  
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DB 237 PSVFLFPPKPKDRLMIKSRTEVTVVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREEQYN 296  
QY 300 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359  
DB 297 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 356

QY 360 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKSRW 419  
DB 357 MTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKSRW 416  
QY 420 QQGNVFCFSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLNGINN 479  
DB 417 QQGNVFCFSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLNGINN 476  
QY 480 YKNPKLTRLMTFFKYPMPKKATELKHLCLEBELKPLEEVNLAKOSKPHLPRDLISIN 539  
DB 477 YKNPKLTRLMTFFKYPMPKKATELKHLCLEBELKPLEEVNLAKOSKPHLPRDLISIN 536  
QY 540 VIVLELKGSETTFMCEVADEATATIVFELNRWITFCQSIISTLT 582  
DB 537 VIVLELKGSETTFMCEVADEATATIVFELNRWITFCQSIISTLT 579

## RESULT 2

US-10-310-719-32  
; Sequence 32, Application US/10310719  
; Publication No. US20030166163A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity  
; FILE REFERENCE: LEX-020  
; CURRENT APPLICATION NUMBER: US/10/310,719  
; CURRENT FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/337,113  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/371,966  
; PRIOR FILING DATE: 2002-04-12  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: di-KS-ala IL2 (D20T) heavy chain fused to IL-2 variant  
US-10-310-719-32

Query Match 89.2%; Score 2738.5; DB 14; Length 579;  
Best Local Similarity 88.3%; Pred. No. 2.8e-166;  
Matches 515; Conservative 30; Mismatches 33; Indels 5; Gaps 2;

QY 1 EVTLVESGGDFVKPGGSLKVSACAAGFAFASHYAMSWVRQTPAKRLIEWAYISSGSGSTYY 60  
DB 1 QIQLVQSGPELKKPGSSVKISCKASGYFTTNYGMNVRQAPGKGLKMWGINTYTGPTY 60  
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTR-VKLGTYVYFDSWGGTTLTVSS 119  
DB 61 ADDFKGRFTITAEITSTLYLQLNLRSEDATATYFCVRFISKGDY---WGQTTVTYSS 116  
QY 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 179  
DB 117 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 176  
QY 180 GLYSLSVVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 239  
DB 177 GLYSLSVVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 236  
QY 240 PSVFLFPPKPKDRLMIKSRTEVTVVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREEQYN 299  
DB 237 PSVFLFPPKPKDRLMIKSRTEVTVVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREEQYN 296  
QY 300 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359  
DB 297 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 356  
QY 360 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKSRW 419  
DB 357 MTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKSRW 416

QY 420 QGNVFCSCVMHEALHNHYTKSLSPGKAPTSSSTKTKTQLQLEHLLDQLMILGINN 479  
Db 417 QGNVFCSCVMHEALHNHYTKSATATPGAAPTSSSTKTKTQLQLEHLLDQLMILGINN 476  
QY 480 YKNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISIN 539  
Db 477 YKNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISIN 536  
QY 540 VIVLELKGSETTFCWEYADETATVIFLNRWITFCOSIISTLT 582  
Db 537 VIVLELKGSETTFCWEYADETATVIFLNRWITFCOSIISTLT 579  
RESULT 3  
US-10-737-208A-6  
; Sequence 6, Application US/10737208A  
; Publication No. US20040203100A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen D.  
; APPLICANT: Lo, Kin-Ming  
; TITLE OF INVENTION: IMMUNOCYTOKINE SEQUENCES AND USES THEREOF  
; FILE REFERENCE: LEX-023  
; CURRENT APPLICATION NUMBER: US/10/737,208A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: US 60/433,945  
; PRIOR FILING DATE: 2002-12-17  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 575  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized Immunoglobulin Heavy Chain-IL-2  
US-10-737-208A-6  
Query Match 88.4%; Score 2715.5; DB 16; Length 575;  
Best Local Similarity 88.8%; Pred. No. 8.1e-165;  
Matches 517; Conservative 24; Mismatches 34; Indels 7; Gaps 3;  
QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAPSHYAMSWVRQTPAKRLIEWAVYISSGGSGTY 60  
Db 1 EVQLVQSGAEVEKPGASVKISCKASGSGFTGYNMNVVRQNIQKSLWGAIDPYYGTSY 60  
QY 61 SDSVKGRTISRDNKNTLYLQMSRLSRSDSAMVFCYTRVKGITYYFDSMGQGTLLTVSSA 120  
Db 61 NQKFKGRLTVDKSTSTAYMHLKLSRSEDATVYICVS---GMEY---NQQGTSTVTVSSA 114  
QY 121 STKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180  
Db 115 STKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 174  
QY 181 LYSLSVTVTPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHCTCPCPAPPELLGGP 240  
Db 175 LYSLSVTVTPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHCTCPCPAPPELLGGP 234  
QY 241 SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 300  
Db 235 SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 294  
QY 301 TYRVSVLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 360  
Db 295 TYRVSVLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 354  
QY 361 TKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 420  
Db 355 TKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 414  
QY 421 QGNVFCSCVMHEALHNHYTKSLSPGKAPTSSSTKTKTQLQLEHLLDQLMILGINN 480  
Db 415 QGNVFCSCVMHEALHNHYTKSLSPG-APTSSSTKTKTQLQLEHLLDQLMILGINN 473  
QY 481 KNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISIN 540

Db 474 KNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISIN 533  
QY 541 VIVLELKGSETTFCWEYADETATVIFLNRWITFCOSIISTLT 582  
Db 534 VIVLELKGSETTFCWEYADETATVIFLNRWITFCOSIISTLT 575  
RESULT 4  
US-10-310-719-37  
; Sequence 37, Application US/10310719  
; Publication No. US20030166163A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity  
; FILE REFERENCE: LEX-020  
; CURRENT APPLICATION NUMBER: US/10/310,719  
; CURRENT FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/337,113  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/371,966  
; PRIOR FILING DATE: 2002-04-12  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37  
; LENGTH: 580  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: dI-NHS76(gamma4h) (FN>AQ) -ala-IL2 (D20T) heavy chain fused to  
; OTHER INFORMATION: IL-2 variant  
US-10-310-719-37  
Query Match 84.4%; Score 2592; DB 14; Length 580;  
Best Local Similarity 84.7%; Pred. No. 6.2e-157;  
Matches 494; Conservative 31; Mismatches 54; Indels 4; Gaps 3;  
QY 1 EVTLVESGGDFVKPGGSLKVS CAASGFAPSHYAMSWVRQTPAKRLIEWAVYISSGGSGTY 59  
Db 1 QVQLQESGPGLVKPSKETLSLTCAVSGYSISSGYWGMIQPPGKGLIEWIGSIYHSGS-TY 59  
QY 60 YSDSVKGRFTISRDNKNTLYLQMSRLSRSDSAMVFCYTRVKGITYYFDSMGQGTLLTVSS 119  
Db 60 YNPSLSKRVITISVDTSKNQFSLKLSVTAADTAIVYICARGKWSK--FDYWGQGTLLTVSS 117  
QY 120 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179  
Db 118 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 177  
QY 180 GLYSLSVTVTPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHCTCPCPAPPELLGG 239  
Db 178 GLYSLSVTVTPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHCTCPCPAPPELLGG 237  
QY 240 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 299  
Db 238 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 297  
QY 300 STYRVSVLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 359  
Db 298 STYRVSVLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 357  
QY 360 LTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 419  
Db 358 LTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 417  
QY 420 QGNVFCSCVMHEALHNHYTKSLSPGKAPTSSSTKTKTQLQLEHLLDQLMILGINN 479  
Db 418 QGNVFCSCVMHEALHNHYTKSATATPGAAPTSSSTKTKTQLQLEHLLDQLMILGINN 477  
QY 480 YKNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISIN 539  
Db 478 YKNPKLTRMLTFFKYPMPKATLKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISIN 537

QY 540 VIVLELKGETTFMCEYADETATVEFLNRWITFCQSIISTLT 582  
DB 538 VIVLELKGETTFMCEYADETATVEFLNRWITFCQSIISTLT 580

RESULT 5  
US-10-310-719-35  
; Sequence 35, Application US/10310719  
; Publication No. US20030166163A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity  
; FILE REFERENCE: LEX-020  
; CURRENT APPLICATION NUMBER: US/10/310,719  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/337,113  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/371,966  
; PRIOR FILING DATE: 2002-04-12  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 35  
; LENGTH: 580  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: dI-NHS76(gamma2h) (FN>AQ) -ala-IL2 (D20T) heavy chain fused to IL2  
; OTHER INFORMATION: variant  
US-10-310-719-35

Query Match 83.4%; Score 2560; DB 14; Length 580;  
Best Local Similarity 84.1%; Pred. No. 6.8e-155;  
Matches 491; Conservative 31; Mismatches 56; Indels 6; Gaps 5;  
QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAFSH-YAMSWVRQTPAKRLEWVAYISSGGSGTY 59  
DB 1 QVQLQESGFLVKPSETLSLTCAVSGYSISSGYWGWRQPPKGLWIGSIYHSGS-TY 59  
QY 60 YSDSVKGRFTISRDNKNTLYLQMSLRSEDSAMFYCTRVKLGTYFYFDSWGGTTLTVSS 119  
DB 60 YNPSLKSRTISVDTSKNQFSLKLSVTAADTAIVYCARQKWSK--FDYWGQGTTLTVSS 117  
QY 120 -ASTKGPSVFPLAPSSKSTSGTAAALCLVDPYFPEPVTVSNWNGALTSGVHTFPAVLQ 178  
DB 118 GASTKGPSVFPLAPCSRSTSESTAALCLVDPYFPEPVTVSNWNGALTSGVHTFPAVLQ 177  
QY 179 SGLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLG 238  
DB 178 SGLYSLSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKVEPKSCDKTHTCPPCPAPP-VA 236  
QY 239 GPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREBOY 298  
DB 237 GPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREBQA 296  
QY 299 NSTYRVSVLTIVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 358  
DB 297 QSTFRVSVLTIVVHODWLNKKEYCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSR 356  
QY 359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSR 418  
DB 357 ENTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPMLDSDGSFFLYSLKLTVDKSR 416  
QY 419 WOQGNVFSCVMHEALHNHYTQKSLSLSPGKAPTSSTSKTKQLQLEHLLDQLMTLNGIN 478  
DB 417 WOQGNVFSCVMHEALHNHYTQKSATATPGAAPTSSSTKTKQLQLEHLLDQLMTLNGIN 476  
QY 479 NYKNPKLTRLTFKPYMPKATLKHQCLREELKPLAEVLNLAOSKNFHLRPRDLISNI 538  
DB 477 NYKNPKLTRLTFKPYMPKATLKHQCLREELKPLAEVLNLAOSKNFHLRPRDLISNI 536  
QY 539 NVIVLELKGETTFMCEYADETATVEFLNRWITFCQSIISTLT 582  
DB 537 NVIVLELKGETTFMCEYADETATVEFLNRWITFCQSIISTLT 580

RESULT 6  
US-10-412-406-32  
; Sequence 32, Application US/10412406  
; Publication No. US20040058394A1  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC.  
; APPLICANT: GABER, Ellen  
; APPLICANT: LYNE, Paul  
; APPLICANT: SALDHANA, Jose W.  
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES  
; FILE REFERENCE: BINA100CN  
; CURRENT APPLICATION NUMBER: US/10/412,406  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: 60/240,285  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/275,289  
; PRIOR FILING DATE: 2001-03-13  
; PRIOR APPLICATION NUMBER: 60/299,987  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: PCT/US01/32140  
; PRIOR FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: RastSEQ for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 663  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-412-406-32

Query Match 72.2%; Score 2218.5; DB 15; Length 663;  
Best Local Similarity 93.1%; Pred. No. 4.7e-133;  
Matches 418; Conservative 9; Mismatches 21; Indels 1; Gaps 1;  
QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAFSH-YAMSWVRQTPAKRLEWVAYISSGGSGTY 60  
DB 215 EVQLVESGGGLVKPGGSLRLSCAASGFTFSYIMYWFQAQPKGLEWATISDGSYTY 274  
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMFYCTRVKLGTYFYFDSWGGTTLTVSS 119  
DB 275 PDSVKGRFTISRDNKNTLYLQMSLRSEDSAMFYCTRVKLGTYFYFDSWGGTTLTVSS 334  
QY 120 ASTKGPSVFPLAPSSKSTSGTAAALCLVDPYFPEPVTVSNWNGALTSGVHTFPAVLQ 179  
DB 335 ASTKGPSVFPLAPSSKSTSGTAAALCLVDPYFPEPVTVSNWNGALTSGVHTFPAVLQ 394  
QY 180 GLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLG 239  
DB 395 GLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLG 454  
QY 240 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREBOY 299  
DB 455 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREBOY 514  
QY 300 STYRVSVLTIVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 359  
DB 515 STYRVSVLTIVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 574  
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRW 419  
DB 575 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRW 634  
QY 420 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 448  
DB 635 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 663

RESULT 7  
US-10-412-406-33  
; Sequence 33, Application US/10412406  
; Publication No. US20040058394A1  
; GENERAL INFORMATION:



; APPLICANT: BIOGEN, INC.  
; APPLICANT: GARBER, Ellen  
; APPLICANT: LYNE, Paul  
; APPLICANT: SALDHANA, Jose W.  
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES  
; FILE REFERENCE: BINA100CN  
; CURRENT APPLICATION NUMBER: US/10/412.406  
; PRIOR FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: 60/240,285  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/275,289  
; PRIOR FILING DATE: 2001-03-13  
; PRIOR APPLICATION NUMBER: 60/299,987  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: PCT/US01/32140  
; PRIOR FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 4852  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-412-406-33

Query Match 72.2%; Score 2218.5; DB 15; Length 4852;  
Best Local Similarity 93.1%; Pred. No. 4.8e-132;  
Matches 418; Conservative 9; Mismatches 21; Indels 1; Gaps 1;

QY	1	EVTLVESGGDFVKPGGSLKVS	CAASGFAPSHYAMSV	VRQTPAKRLEWVA	ISSGGSGTY	60			
DB	4404	EVOLVEGGDLVKPGGSLKLS	CAASGFTFSYYMYFR	QAPGKLEWVA	ISDGGSYTY	4463			
QY	61	SDSVKGRFTISRDNAXNTLY	LQMRSLRSEDSAMY	FCTRVKLG	TYFDSMGQGT	119			
DB	4464	PDSVKGRFTISRDNAXNSLY	LQMSLRRAEDATY	YCARENGFY	FDYWGQGT	4523			
QY	120	ASTKGPSPVPLAPSSKTS	GGTAALGCLVKDY	PEPVTVMNSGALT	SGVHTFP	PAVLQSS	179		
DB	4524	ASTKGPSPVPLAPSSKTS	GGTAALGCLVKDY	PEPVTVMNSGALT	SGVHTFP	PAVLQSS	4583		
QY	180	GLYSLSVTVPSSSLG	TQTYICNVNHPKSN	TKVDKVPKSCDK	THTCPP	APPELLGG	239		
DB	4584	GLYSLSVTVPSSSLG	TQTYICNVNHPKSN	TKVDKVPKSCDK	THTCPP	APPELLGG	4643		
QY	240	PSVFLPPPKD	TLMSRTP	PEVTCVVVDVSHED	PEVKFNWY	DGVEVHNAKTK	PREEQYN	299	
DB	4644	PSVFLPPPKD	TLMSRTP	PEVTCVVVDVSHED	PEVKFNWY	DGVEVHNAKTK	PREEQYN	4703	
QY	300	STYRVVSVLT	VLHQLDMLNG	KEYCKVSNKAL	PAPIETK	ISKAKGQ	PREPQVY	TLPPSRDE	359
DB	4704	STYRVVSVLT	VLHQLDMLNG	KEYCKVSNKAL	PAPIETK	ISKAKGQ	PREPQVY	TLPPSRDE	4763
QY	360	LTKNQVSLTCLVKGF	PSDIAVEWESNG	QPENNYK	TTTPVLD	SDGSF	FLYSKL	TVDKSRW	419
DB	4764	LTKNQVSLTCLVKGF	PSDIAVEWESNG	QPENNYK	TTTPVLD	SDGSF	FLYSKL	TVDKSRW	4823
QY	420	QQGNVFSCSVMHEAL	HNHYTQKSLS	LSPG	448				
DB	4824	QQGNVFSCSVMHEAL	HNHYTQKSLS	LSPG	4852				

RESULT 8  
US-10-679-620-64  
; Sequence 64, Application US/10679620  
; Publication No. US20040110930A1  
; GENERAL INFORMATION:  
; APPLICANT: Large Scale Biology  
; APPLICANT: Reini, Stephen J.  
; APPLICANT: Edwards, Patricia C.  
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING  
; FILE REFERENCE: 34150-004A  
; CURRENT APPLICATION NUMBER: US/10/679, 620  
; CURRENT FILING DATE: 2003-10-03

; PRIOR APPLICATION NUMBER: 60/415,940  
; PRIOR FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 64  
; LENGTH: 713  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: p9E10chimericv2-1, see Example 15  
US-10-679-620-64

Query Match 72.2%; Score 2216; DB 16; Length 713;  
Best Local Similarity 91.7%; Pred. No. 7.4e-133;  
Matches 419; Conservative 10; Mismatches 20; Indels 8; Gaps 2;

QY	1	EVTLVESGGDFVKPGGSLKVS	CAASGFAPSHYAMSV	VRQTPAKRLEWVA	ISSGGSGTY	60			
DB	257	EVDLVESGGDLVKPGGSLKLS	CAASGFTFSHYGMSV	VRQTPDKRLEWVA	TIGSRGT	316			
QY	61	SDSVKGRFTISRDNAXNTLY	LQMRSLRSEDSAMY	FCTRVK	LT---	DSMGQ	112		
DB	317	PDSVKGRFTISRDNAXNLY	LQMSLKSEDTANY	YCARRSEF	YVYNGTY	YSAMDY	WGQ	376	
QY	113	TTLTVSSASTKGPSPVPL	APSSKTSGGTAALG	CLVKDY	PEPVTVMNSGALT	SGVHTF	172		
DB	377	ASVTSSASTKGPSPVPL	APSSKTSGGTAALG	CLVKDY	PEPVTVMNSGALT	SGVHTF	436		
QY	173	PAVLQSSGLYSLSVTV	PSSSLG	TQTYICNVNHPKSN	TKVDKVPKSCDK	THTCPP	232		
DB	437	PAVLQSSGLYSLSVTV	PSSSLG	TQTYICNVNHPKSN	TKVDKVPKSCDK	THTCPP	496		
QY	233	APPELLGGSPVFLPP	PKD	TLMSRTP	PEVTCVVVDVSHED	PEVKFNWY	DGVEVHNAKTK	292	
DB	497	APPELLGGSPVFLPP	PKD	TLMSRTP	PEVTCVVVDVSHED	PEVKFNWY	DGVEVHNAKTK	556	
QY	293	PREEQYNSTYRVVSV	LT	VLHQLDMLNG	KEYCKVSNKAL	PAPIETK	ISKAKGQ	PREPQVY	352
DB	557	PREEQYNSTYRVVSV	LT	VLHQLDMLNG	KEYCKVSNKAL	PAPIETK	ISKAKGQ	PREPQVY	616
QY	353	LPSPRDELTKNQVSL	TCLVKGF	PSDIAVEWESNG	QPENNYK	TTTPVLD	SDGSF	FLYSKL	412
DB	617	LPSPRDELTKNQVSL	TCLVKGF	PSDIAVEWESNG	QPENNYK	TTTPVLD	SDGSF	FLYSKL	676
QY	413	TVDKSRWQQGNVF	SCSVMHEAL	HNHYTQKSLS	LSPG	449			
DB	677	TVDKSRWQQGNVF	SCSVMHEAL	HNHYTQKSLS	LSPG	713			

RESULT 9  
US-10-679-620-62  
; Sequence 62, Application US/10679620  
; Publication No. US20040110930A1  
; GENERAL INFORMATION:  
; APPLICANT: Large Scale Biology  
; APPLICANT: Reini, Stephen J.  
; APPLICANT: Edwards, Patricia C.  
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING  
; FILE REFERENCE: 34150-004A  
; CURRENT APPLICATION NUMBER: US/10/679, 620  
; CURRENT FILING DATE: 2003-10-03  
; PRIOR APPLICATION NUMBER: 60/415,940  
; PRIOR FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 62  
; LENGTH: 715  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: p9E10chimericv1-1, see Example 15  
US-10-679-620-62

```
Query Match      72.2%; Score 2216; DB 16; Length 715;
Best Local Similarity 91.7%; Pred. No. 7.4e-133;
Matches 419; Conservative 10; Mismatches 20; Indels 8; Gaps 2;

QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAPAFSHYAMSWVRQTTPAKRLIEWAYISSGGSGTY 60
DB EVDLVESGGDLVKPGGSLKLSAAAGFTFSHYGMSWVRQTPDKRLIEWATIGSRGTYY 318
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTYYFDGSGOQTTLTVSSA 112
DB PDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTYYFDGSGOQTTLTVSSA 378
QY 113 TTLTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPPEPVTVSNWNGALTSVGH 172
DB ASVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPPEPVTVSNWNGALTSVGH 438
QY 173 PAVLOSSGLYSLSSVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCP 232
DB PAVLOSSGLYSLSSVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCP 498
QY 233 APELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 292
DB APELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 558
QY 293 PREEOYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 352
DB PREEOYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 618
QY 353 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 412
DB LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 678
QY 413 TVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
DB TVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 715

RESULT 10
US-10-938-353-102
; Sequence 102, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
; APPLICANT: BEDIA, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
; APPLICANT: FOLTZ, IAN
; APPLICANT: HAAK-FRENSCH, MARY
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: LOW, JOSEPH EDWIN
; APPLICANT: MOBLEY, JAMES LESLIE
; TITLE OF INVENTION: ANTIBODIES TO M-CSF
; FILE REFERENCE: ABX-PF4
; CURRENT APPLICATION NUMBER: US/10/938,353
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/502,163
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 102
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-353-102

Query Match      71.8%; Score 2205; DB 17; Length 464;
Best Local Similarity 92.2%; Pred. No. 2.2e-132;
Matches 414; Conservative 12; Mismatches 19; Indels 4; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAPAFSHYAMSWVRQTTPAKRLIEWAYISSGG 60
DB 20 QVQLVESGGGLVKPGGSLRLSAAAGFTFSHYMSWVRQTPAKRLIEWAYISSGGSTI 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTYYFDGSGOQTTLT 120

Query Match      71.7%; Score 2201.5; DB 15; Length 447;
Best Local Similarity 92.9%; Pred. No. 3.6e-132;
Matches 416; Conservative 9; Mismatches 22; Indels 1; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAPAFSHYAMSWVRQTTPAKRLIEWAYISSGG 60
DB 1 EVQLVESGGGLVQPGGSLRLSAAAGFTFSRYTMSWVRQAPGKGLIEWATISGGGH-T 59
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTYYFDGSGOQTTLT 120
DB 60 LDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTYYFDGSGOQTTLT 119
QY 121 STKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPPEPVTVSNWNGALTSVGH 180
DB 120 STKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPPEPVTVSNWNGALTSVGH 179
QY 181 LYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCP 240
DB 180 LYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCP 239
QY 241 SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 300
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DB 80 ADSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTYYFDGSGOQTTLT 135
QY 121 STKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPPEPVTVSNWNGALTSVGH 180
DB 136 STKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPPEPVTVSNWNGALTSVGH 195
QY 181 LYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCP 240
DB 196 LYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCP 255
QY 241 SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 300
DB 256 SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 315
QY 301 TYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 360
DB 316 TYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 375
QY 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 420
DB 376 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 435
QY 421 QGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
DB 436 QGNVFCSCVMHEALHNHYTQKSLSLSPGK 464

RESULT 11
US-10-474-832-4
; Sequence 4, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: ANTIBODIES TO VLA-1
; FILE REFERENCE: A101 PCT
; CURRENT APPLICATION NUMBER: US/10/474,832
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/283,794
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/303,689
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-474-832-4

Query Match      71.7%; Score 2201.5; DB 15; Length 447;
Best Local Similarity 92.9%; Pred. No. 3.6e-132;
Matches 416; Conservative 9; Mismatches 22; Indels 1; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAPAFSHYAMSWVRQTTPAKRLIEWAYISSGG 60
DB 1 EVQLVESGGGLVQPGGSLRLSAAAGFTFSRYTMSWVRQAPGKGLIEWATISGGGH-T 59
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTYYFDGSGOQTTLT 120
DB 60 LDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLTYYFDGSGOQTTLT 119
QY 121 STKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPPEPVTVSNWNGALTSVGH 180
DB 120 STKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPPEPVTVSNWNGALTSVGH 179
QY 181 LYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCP 240
DB 180 LYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCP 239
QY 241 SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 300
```

Db 240 SVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299  
QY 301 TYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPPQVYITLPPSRDEL 360  
Db 300 TYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPPQVYITLPPSRDEL 359  
QY 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420  
Db 360 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 419  
QY 421 QGNVFSCSVNHEALHNHYTQKSLSLSPG 448  
Db 420 QGNVFSCSVNHEALHNHYTQKSLSLSPG 447

RESULT 12  
US-10-150-475A-6  
; Sequence 6, Application US/10150475A  
; Publication No. US20030103985A1  
; GENERAL INFORMATION:  
; APPLICANT: Adolf, G. et al.  
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates  
; FILE REFERENCE: 1/1211  
; CURRENT APPLICATION NUMBER: US/10/150,475A  
; PRIOR FILING DATE: 2002-05-17  
; PRIOR APPLICATION NUMBER: US 60/307,451  
; PRIOR FILING DATE: 2001-07-24  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Humanised  
; OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 6  
US-10-150-475A-6

Query Match 71.7%; Score 2200.5; DB 14; Length 444;  
Best Local Similarity 92.4%; Pred. No. 4.1e-132;  
Matches 415; Conservative 11; Mismatches 18; Indels 5; Gaps 1;

QY 1 EYTLVESGGDFVKPGGSLKVS CAASGFAPFASHYAMSWVRQTPAKRLWVAYISSGGSTYY 60  
Db 1 EVQLVESGGGLVKPGGSLRLS CAASGFTFSSYDMSWVRQAPGKLEWVSTISSGGSYTY 60  
QY 61 SDSVKGRTISRDNKNTLYLQWRSLSRSDSAMYFCTRVKLGTYYPDSWGQGTTLTVSSA 120  
Db 61 LOSIKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCARQGL-----DYMGRGTLTVSSA 115  
QY 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180  
Db 116 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 175  
QY 181 LYSLSVSVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 240  
Db 176 LYSLSVSVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 235  
QY 241 SVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300  
Db 236 SVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 295  
QY 301 TYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPPQVYITLPPSRDEL 360  
Db 296 TYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPPQVYITLPPSRDEL 355  
QY 421 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420  
Db 356 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 415  
QY 421 QGNVFSCSVNHEALHNHYTQKSLSLSPG 449  
Db 420 QGNVFSCSVNHEALHNHYTQKSLSLSPG 448

Db 416 QGNVFSCSVNHEALHNHYTQKSLSLSPGK 444

RESULT 13  
US-10-704-522-6  
; Sequence 6, Application US/10704522  
; Publication No. US20040120949A1  
; GENERAL INFORMATION:  
; APPLICANT: Adolf, Gunther  
; APPLICANT: Baumann, Michael  
; APPLICANT: Heider, Karl-Heinz  
; TITLE OF INVENTION: Compositions and methods for treating cancer using  
; FILE REFERENCE: 1/1414  
; CURRENT APPLICATION NUMBER: US/10/704,522  
; CURRENT FILING DATE: 2003-11-07  
; PRIOR APPLICATION NUMBER: US 60/429,516  
; PRIOR FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: EP 02024881  
; PRIOR FILING DATE: 2002-11-08  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain  
US-10-704-522-6

Query Match 71.7%; Score 2200.5; DB 16; Length 444;  
Best Local Similarity 92.4%; Pred. No. 4.1e-132;  
Matches 415; Conservative 11; Mismatches 18; Indels 5; Gaps 1;

QY 1 EYTLVESGGDFVKPGGSLKVS CAASGFAPFASHYAMSWVRQTPAKRLWVAYISSGGSTYY 60  
Db 1 EVQLVESGGGLVKPGGSLRLS CAASGFTFSSYDMSWVRQAPGKLEWVSTISSGGSYTY 60  
QY 61 SDSVKGRTISRDNKNTLYLQWRSLSRSDSAMYFCTRVKLGTYYPDSWGQGTTLTVSSA 120  
Db 61 LOSIKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCARQGL-----DYMGRGTLTVSSA 115  
QY 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180  
Db 116 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 175  
QY 181 LYSLSVSVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 240  
Db 176 LYSLSVSVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 235  
QY 241 SVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300  
Db 236 SVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 295  
QY 301 TYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPPQVYITLPPSRDEL 360  
Db 296 TYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPPQVYITLPPSRDEL 355  
QY 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420  
Db 356 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 415  
QY 421 QGNVFSCSVNHEALHNHYTQKSLSLSPGK 449  
Db 416 QGNVFSCSVNHEALHNHYTQKSLSLSPGK 444

RESULT 14  
US-10-645-215-6  
; Sequence 6, Application US/10645215  
; Publication No. US20040126379A1  
; GENERAL INFORMATION:  
; APPLICANT: Adolf, Gunther



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:58:15 ; Search time 32.9571 Seconds  
(without alignments)  
1699.125 Million cell updates/sec

Title: US-10-089-500-57

Perfect score: 3071

Sequence: 1 EVTLVESGGDFVKPGSLKV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1767	57.5	330	1 GHU	Ig gamma-1 chain C
2	1630.5	53.1	377	2 A23511	Ig gamma-3 chain C
3	1628.5	53.0	377	2 A60764	Ig gamma-3 chain C
4	1604	52.2	326	1 G2HU	Ig gamma-4 chain C
5	1590.5	51.8	327	1 G4HU	Ig gamma-4 chain C
6	1507.5	49.1	444	2 PC4436	Ig gamma-2 chain C
7	1466	47.7	470	2 S22080	Ig heavy chain pre
8	1430.5	46.6	469	2 S37483	Ig gamma-2a chain
9	1423	46.3	374	2 S69339	Ig heavy chain V r
10	1421	46.3	446	2 S40295	Ig gamma-2a chain
11	1412	46.0	472	2 G31459	Ig gamma-1 chain -
12	1365	44.4	474	1 G2MS11	Ig gamma-2b chain
13	1343.5	43.7	475	2 S01321	Ig gamma-2b chain
14	1263	41.1	328	2 I47159	Ig gamma-2a chain
15	1260	41.0	255	4 S31866	Ig gamma-1 chain C
16	1257	40.9	328	2 I47160	Ig gamma 2b chain
17	1254	40.8	234	2 PT0207	Ig gamma chain C r
18	1231	40.1	328	2 I47158	Ig gamma 1 chain C
19	1230.5	40.1	323	1 GHRB	Ig gamma chain C r
20	1227	40.0	328	2 I47161	Ig gamma 3 chain C
21	1216.5	39.6	329	1 G2GP	Ig gamma-2 chain C
22	1161.5	37.8	308	2 C30554	Ig heavy chain C r
23	1152	37.5	326	2 PS0017	Ig gamma-1 chain C
24	1151	37.5	289	1 G3H0W1	Ig gamma-3 heavy c
25	1146.5	37.3	333	2 PS0018	Ig gamma-2b chain
26	1142	37.2	324	1 G1MS	Ig gamma-1 chain C
27	1141	37.2	329	1 G3MSC	Ig gamma-3 chain C
28	1139	37.1	393	1 G1MSM	Ig gamma-1 chain C
29	1130	36.8	398	1 G3MSM	Ig gamma-3 chain C

30	1126	36.7	330	1 G2MSA	Ig gamma-2a chain
31	1123.5	36.6	335	1 G2MSAB	Ig gamma-2a chain
32	1121	36.5	399	1 G2MSAM	Ig gamma-2a chain
33	1118.5	36.4	329	2 S00847	Ig gamma-2c chain
34	1118	36.4	548	2 S38864	Ig epsilon chain C
35	1112	36.2	322	2 PS0019	Ig gamma-2a chain
36	1092.5	35.6	327	2 S06611	Ig gamma-2b chain
37	1082	35.2	405	1 G2MSBM	Ig gamma-2b chain
38	1066	34.7	277	2 I47162	Ig gamma 4 chain c
39	845.5	27.5	549	2 S04845	Ig heavy chain pre
40	817.5	26.6	249	2 S69340	Ig heavy chain VHI
41	802.5	26.1	572	2 B46529	Ig heavy chain (
42	801.5	26.1	241	2 S69131	Ig heavy chain (DO
43	770	25.1	218	2 A36040	Ig heavy chain V-I
44	760	24.7	220	2 A49444	Ig gamma-1 heavy c
45	744.5	24.2	254	2 B31790	Ig heavy chain V r
46	740.5	24.1	213	2 S68213	Ig heavy chain (Ma
47	734	23.9	246	2 S38950	Ig gamma chain - m
48	731	23.8	627	2 I46883	Ig mu chain precu
49	707	23.0	180	2 I46732	Ig gamma heavy cha
50	695.5	22.6	585	2 A46507	Ig alpha chain - c
51	690	22.5	153	1 ICG12	interleukin-2 prec
52	690	22.5	153	1 ICHU2	interleukin-2 prec
53	686	22.3	220	2 S68211	Ig heavy chain (Ma
54	665.5	21.7	592	2 S25705	Ig mu chain - sh
55	652	21.2	231	2 PC4155	Ig gamma-2b chain
56	648.5	21.1	568	2 A34891	Ig heavy chain pre
57	640	20.8	214	2 PC4202	monoclonal antibod
58	637	20.7	577	2 I50731	Ig heavy chain - n
59	620.5	20.2	221	2 S49220	Ig gamma-1 chain -
60	604	19.7	504	2 S00390	Ig gamma chain (cl
61	587	19.1	509	2 S17597	Ig delta chain (WI
62	573.5	18.7	568	2 A45804	Ig mu chain C regi
63	571	18.6	152	2 S14236	Ig gamma-1 chain C
64	547	17.8	143	2 S23624	Ig heavy chain V r
65	534.5	17.4	154	2 JN0698	interleukin 2 prec
66	534	17.4	342	2 A46529	Ig gamma chain (5.
67	528	17.2	170	2 A35944	Ig gamma-2a chain
68	516.5	16.8	573	2 S12838	Ig mu chain precu
69	509.5	16.6	448	2 S03186	Ig heavy chain C r
70	492	16.0	428	1 EHHU	Ig epsilon chain C
71	490	16.0	97	2 S26652	Ig gamma-1 chain C
72	486	15.8	429	1 EHRT	Ig epsilon-chain -
73	485.5	15.8	426	2 I36948	interleukin-2 - Mo
74	482.5	15.7	155	2 S33509	anti-peptide Fab'
75	479	15.6	119	2 B34353	interleukin-2 prec
76	478.5	15.6	154	2 S16241	Ig heavy chain pre
77	478	15.6	152	2 B26471	Ig heavy chain, se
78	478	15.6	580	2 A46538	Ig heavy chain V r
79	471	15.3	120	2 S55536	Ig heavy chain V r
80	470.5	15.3	121	2 I27887	Ig heavy chain V r
81	469.5	15.3	433	2 S31436	Ig upailon chain -
82	469	15.3	120	2 S55537	Ig heavy chain V r
83	469	15.3	122	2 E27888	Ig heavy chain V r
84	469	15.3	149	2 S31391	interleukin-2 prec
85	467	15.2	111	2 PH1007	Ig heavy chain V r
86	467	15.2	160	2 S05271	Ig heavy chain pre
87	466.5	15.2	118	2 PH0097	Ig heavy chain V r
88	466.5	15.2	119	2 F27888	Ig heavy chain V r
89	464	15.1	138	2 S09258	Ig heavy chain V r
90	463	15.1	120	2 S55539	Ig heavy chain V r
91	462	15.0	117	2 S20641	Ig heavy chain V r
92	461	15.0	117	2 PL0249	Ig heavy chain V r
93	460.5	15.0	118	2 PH0096	Ig heavy chain V r
94	460	15.0	120	2 S55538	Ig heavy chain V r
95	457	14.9	1005	2 T18537	Ig heavy chain - c
96	456	14.8	119	2 S31107	Ig heavy chain - h
97	456	14.8	124	2 C27888	Ig heavy chain V r
98	456	14.8	138	2 S31666	Ig heavy chain V r
99	455.5	14.8	112	2 S26327	Ig heavy chain V r
100	455.5	14.8	147	2 I37780	Ig variable region

## ALIGNMENTS

## RESULT 1

GHU  
Ig gamma-1 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Jan-1981 #sequence\_revision 18-Aug-1992 #text\_change 09-Jul-2004  
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146  
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982  
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.  
A:Reference number: A93433; MUID:82274238; PMID:6287432  
A:Accession: A93433  
A:Molecule type: DNA  
A:Residues: 1-330 <ELL>  
A:CROSS-references: UNIPROT:P01857; EMBL:217370  
A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,  
A:Note: Lys-330 is removed after translation  
R:Harris, L.J.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S33904  
A:Accession: S36861  
A:Molecule type: DNA  
A:Residues: 2-330 <HAR>  
A:CROSS-references: EMBL:217370  
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.  
Cell 29, 671-679, 1982  
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a  
A:Reference number: S33887; MUID:83001943; PMID:6811139  
A:Accession: S33887  
A:Molecule type: DNA  
A:Residues: 88-113;235-330 <TAK>  
A:CROSS-references: EMBL:217370  
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,  
Biochemistry 9, 3161-3170, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen  
A:Reference number: A90563; MUID:71064024; PMID:5489771  
A:Contents: myeloma protein Eu  
A:Accession: B90563  
A:Molecule type: protein  
A:Residues: 1-96, 'R', 98-135 <CUN>  
A:Note: this sequence has the G1m(3) marker, 97-Arg  
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen  
A:Reference number: A90564; MUID:71064025; PMID:5530842  
A:Contents: Eu  
A:Accession: A90564  
A:Molecule type: protein  
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,  
A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met  
R:Ponstingl, H.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),  
igen Primärstruktur.  
A:Reference number: A91668; MUID:77070269; PMID:826475  
A:Contents: myeloma protein Nie  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27  
A:Note: this sequence has the G1m(17) and G1m(1) markers  
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A:Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI  
A:Reference number: A91723; MUID:83289131; PMID:6884994  
A:Contents: myeloma protein KOL; disulfide bonds  
A:Accession: A91723  
A:Molecule type: protein  
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH  
A:Note: this sequence has the G1m(3) and G1m(non-1) markers  
R:Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide  
A:Reference number: A90565; MUID:71064027; PMID:4923144  
A:Contents: annotation; disulfide bonds  
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglobuli  
enbromide cleavage products, and the disulfide bridges.  
A:Reference number: A91667; MUID:77070267; PMID:1002129  
A:Contents: annotation; disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG1  
A:CROSS-references: GDB:120085; OMIM:147100  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 114/1; 224/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)  
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into lai  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:137-206/Domain: immunoglobulin homology <IM2>  
F:243-310/Domain: immunoglobulin homology <IM3>  
F:27-83,144-204,250-308/Disulfide bonds: #status experimental  
F:103/Disulfide bonds: interchain (to light chain) #status experimental  
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental  
Query Match 57.5%; Score 1767; DB 1; Length 330;  
Best Local Similarity 100.0%; Pred. No. 2.6e-92;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 120 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179  
DB 1 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
QY 180 GLYSLSVVTVTPSSSLGTTQYICNVNHPKSTKVDKKVEPKSCDKHTHTCPCPAPELGG 239  
DB 61 GLYSLSVVTVTPSSSLGTTQYICNVNHPKSTKVDKKVEPKSCDKHTHTCPCPAPELGG 120  
QY 240 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEQYN 299  
DB 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEQYN 180  
QY 300 STYRVSVLTVLDHDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359  
DB 181 STYRVSVLTVLDHDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 419  
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 300  
QY 420 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 449  
DB 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330  
RESULT 2  
A23511  
Ig gamma-3 chain C region (allotype G3m(b)) - human  
C:Species: Homo sapiens (man)  
C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
C:Accession: A23511  
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
Nucleic Acids Res. 14, 1779-1789, 1986  
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: con  
A:Reference number: A23511; MUID:86148507; PMID:3081877  
A:Accession: A23511  
A:Molecule type: DNA  
A:Residues: 1-377 <HUC>  
A:CROSS-references: GB:X03604; GB:M12958; NID:G33070; PIDN:CAA27268.1; PID:G577056  
C:Genetics:  
A:Gene: GDB:IGHG3  
A:CROSS-references: GDB:119339; OMIM:147120  
A:Map position: 14q32.33-14q32.33





A;Contents: annotation; Sa, disulfide bonds

C;Genetics:

A;Gene: GDB:IGHG2

A;Cross-references: GDB:119338; OMIM:147110

A;Map position: 14q32.33-14q32.33

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:133-202/Domain: immunoglobulin homology <IM2>

F:239-306/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (co light chain) #status experimental

F:127-83,140-200,246-304/Disulfide bonds: #status experimental

F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.2%; Score 1604; DB 1; Length 326;  
Best Local Similarity 91.2%; Pred. No. 3.7e-83;  
Matches 301; Conservative 12; Mismatches 13; Indels 4; Gaps 2;

QY 120 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179  
DB 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCTPCCPAPPELLGG 239  
DB 61 GLYSLSSVVTVPSSNFGTQTYTCNVNDRKPSNTKVDKTKVERKCCVE- --CPPCPAPP- VAG 116

QY 240 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 299  
DB 117 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREEOFN 176

QY 300 STYRVSVSLTVLHVDWLNKGEYKCKVSNKALPAPIETKISKAGQRPQVYVTLPPSRDE 359  
DB 177 STFRVSVSLTVLHVDWLNKGEYKCKVSNKGLPAPIETKISKAGQRPQVYVTLPPSRDE 236

QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVDKSRW 419  
DB 237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVDKSRW 296

QY 420 OQGNVFCSCVMHEALHNHYTKLSLSPGK 449  
DB 297 OQGNVFCSCVMHEALHNHYTKLSLSPGK 326

#### RESULT 5

G4HU

Ig gamma-4 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004

C;Accession: A90933; A90249; A02150

R;Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A;Reference number: A90933; MUID:83157104; PMID:6299662

A;Accession: A90933

A;Molecule type: DNA

A;Residues: 1-327 <ELL>

A;Cross-references: UNIPROT:P01861

A;Note: the sequence was determined from the germline gene

R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant

A;Reference number: A90249; MUID:70207560; PMID:4192699

A;Accession: A90249

A;Molecule type: protein

A;Residues: 1-30;81-326 <PIN>

C;Genetics:

A;Gene: GDB:IGHG4

A;Cross-references: GDB:119340; OMIM:147130

A;Map position: 14q32.33-14q32.33

A;Introns: 99/1, 111/1, 221/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:127-83,141-201,247-305/Disulfide bonds: #status predicted

F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.8%; Score 1590.5; DB 1; Length 327;  
Best Local Similarity 90.9%; Pred. No. 2.1e-82;  
Matches 300; Conservative 12; Mismatches 15; Indels 3; Gaps 1;

QY 120 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179  
DB 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCTPCCPAPPELLGG 239  
DB 61 GLYSLSSVVTVPSSSLGTQTYTCNVNDRKPSNTKVDKRVESK- --YGPCCPCPAPEFLGG 117

QY 240 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 299  
DB 118 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREEOFN 177

QY 300 STYRVSVSLTVLHVDWLNKGEYKCKVSNKALPAPIETKISKAGQRPQVYVTLPPSRDE 359  
DB 178 STYRVSVSLTVLHVDWLNKGEYKCKVSNKGLPAPIETKISKAGQRPQVYVTLPPSQEE 237

QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVDKSRW 419  
DB 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVDKSRW 297

QY 420 OQGNVFCSCVMHEALHNHYTKLSLSPGK 449  
DB 298 OQGNVFCSCVMHEALHNHYTKLSLSPGK 327

#### RESULT 6

PC4436

monoclonal antibody 13-1 heavy chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000

C;Accession: PC4436

R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.;

Biochem. Biophys. Res. Commun. 240, 566-572, 1997

A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin

A;Reference number: JC5810; MUID:98063277; PMID:9398605

A;Accession: PC4436

A;Molecule type: protein

A;Residues: 1-444 <AKA>

C;Comment: This catalytic antibody has peroxidase oxidase activity. It is directed again

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F:251-320/Domain: immunoglobulin homology <IMW>

F:22/Disulfide bonds: interchain (to 98) #status predicted

F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 49.1%; Score 1507.5; DB 2; Length 444;  
Best Local Similarity 60.9%; Pred. No. 1.4e-77;  
Matches 276; Conservative 74; Mismatches 90; Indels 13; Gaps 6;

QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAFSAHYAMSWRQTQPAKRLWEVAYIS- --SGSGGT 58  
DB 1 EVQXVETGGGLVRFPGNSLKLSCLTSGFTFSNYRHWLQPPGKRLWIAVITKSDNYGA 60

QY 59 YYSDSVKGRTTISRDNKNTLYLQWRSLSRSDSAMYFCTRVKLGTYYFDSCQGTTLTVS 118  
DB 61 KYAESVGRFTISRDSKSSVYLQWNLRLREEDTATYYCCRTTP- WYIAMDQCGQGTSVIVS 119



Qy 119 SASTKGPSVPLAPSSKSTSGTAAALCLVKDTPPEPVTVSWNSGALTSVHTFPVAVLQS 178  
Db 120 SAKTTPSVPLAPSGSAQAQTNNMTLGLCKVGFPEPEPVTVWNSGLSSGVHTFPVAVLQS 179  
Qy 179 SGYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVBPCKSDKTHTCPP--CPAPEL 236  
Db 180 D-LYTLSSSVTVPSSTWPESETVCNVAHPASSTKVDKIVPRDCG---CKPCICTVPEV 234  
Qy 237 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNNAKTPREE 296  
Db 235 ---SSVFIFPPPKDPTLTITLTPKVTCTVVDVSHEDPEVKFNMYVDGVEVHNNAKTPREE 291  
Qy 297 QYNSTYRVVSVLTVLHQDLNMEKEEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 356  
Db 292 QFNSTFRSVBELPTMHQDNLNMEKEEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 351  
Qy 357 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDK 416  
Db 352 KEQWAKDKVSLTCHITDFFPEDITVEWQWNGQPENNYKTTPPVLDSDGSFPLYSKLTVDK 411  
Qy 417 SRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 449  
Db 412 SNWEGNTFTCSVLHLEGLHNHTYTKSLSPGK 444

## RESULT 7

S22080

Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine

N/Alternate names: Ig gamma-1 chain C region (clone 8.10)

C/Species: Bos primigenius taurus (cattle)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C/Accession: S22080; S06610; A31303

R/Sanders, P.G.

submitted to the EMBL Data Library, November 1991

A/Reference number: S22080

A/Accession: S22080

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-470 &lt;SAN&gt;

A/Cross-references: EMBL:X62916; NID:G439; PIDN:CAA44699.1; PID:G440

R/Symons, D.B.A.; Clarkson, C.A.; Beale, D.

Mol. Immunol. 26, 841-850, 1989

A/Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma

A/Reference number: S06610; MUID:90097956; PMID:2513487

A/Accession: S06610

A/Molecule type: DNA

A/Residues: 142-470 &lt;SYM&gt;

A/Cross-references: EMBL:X16701

A/Note: the sequence was determined from the germline gene

C/Genetics:

A/Gene: Ig CH gamma-1

A/Introns: 98/1; 111/1; 221/1

A/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein

F;161-225/Domain: immunoglobulin homology &lt;IMM&gt;

F;318/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 47.7%; Score 1466; DB 2; Length 470;

Best Local Similarity 61.5%; Pred. No. 3.3e-75;

Matches 280; Conservative 60; Mismatches 105; Indels 10; Gaps 6;

Qy 1 EVTLVESGGDFVKPGGSLKVSQAASGFARSHYAMSVWRTPAKRLWVAYISSGSGTYY 60

Db 20 QVQLRESGSLVKPSQTLSTCTVSGFSLSSYALTWRQAPGALEWVGITSGGT-TYY 78

Qy 61 SDSVKGRTISRDNKNTLYLQNRSLRSDSAMYFCTRVKLGTY-----YFDSHGQGTTLT 116

Db 79 NPALKSLRSLTKENSKQVSLSSVSTPTDATTYYCARSTYGVSGDGAIDAWGQGLVLT 138

Qy 117 VSSASTKGPSVPLAPSSKSTSGTAAALCLVKDTPPEPVTVSWNSGALTSVHTFPVAVL 176

Db 139 VSSASTAPKVPYPLSSCCGDKSSSTVTLGLCLVSNYSMPPEPVTVWNSGALKSGVHTFPVAVL 198

Qy 177 QSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVBPCKSDKTHTCPPCPAPEL 236  
Db 199 QSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVBPCKSDKTHTCPPCPAPEL 255  
Qy 237 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNNAKTPREE 296  
Db 256 PGSPSVFIIPPKDPTLTITLTPKVTCTVVDVSHEDPEVKFNMYVDGVEVHNNAKTPREE 315  
Qy 297 QYNSTYRVVSVLTVLHQDLNMEKEEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 356  
Db 316 QFNSTYRVVSVLTVLHQDLNMEKEEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 375  
Qy 357 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDK 414  
Db 376 QEELSKSTVSLTCHITDFFPEDITVEWQWNGQPENNYKTTPPVLDSDGSFPLYSKLTVDK 435  
Qy 415 DKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 449  
Db 436 DRNSWQEGDPTTCVMHEALHNHYTQKSLSLSPGK 470

## RESULT 8

S37483

Ig gamma-2a chain - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C/Accession: S37483

R/Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993

A/Reference number: S37483

A/Accession: S37483

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-469 &lt;DUC&gt;

A/Cross-references: EMBL:X70423; NID:G406252; PIDN:CAA49868.1; PID:G406253

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: immunoglobulin

F;276-345/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 46.6%; Score 1430.5; DB 2; Length 469;

Best Local Similarity 58.8%; Pred. No. 3.2e-73;

Matches 266; Conservative 71; Mismatches 110; Indels 5; Gaps 4;

Qy 1 EVTLVESGGDFVKPGGSLKVSQAASGFARSHYAMSVWRTPAKRLWVAYISSGSGTYY 60

Db 20 QIQLQSGPELVKPGASVKISCKASGYTFTDYINWVKQKPGQGLKAWIGWIYPASGNTKY 79

Qy 61 SDSVKGRTISRDNKNTLYLQNRSLRSDSAMYFCTRVKLGTY-----YFDSHGQGTTLTVSS 119

Db 80 NENFKGKATLTVDTSSTAYMQLSLTSBTDATVYFCARAMGATATLLDYWGQGTTLTVSS 139

Qy 120 ASTKGPSVPLAPSSKSTSGTAAALCLVKDTPPEPVTVSWNSGALTSVHTFPVAVLQS 179

Db 140 AKTTAPSVPLAPVCGDITGSSVTGLCLVKGFPEPEPVTVWNSGSLSSGVHTFPVAVLQSD 199

Qy 180 GLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVBPCKSDKTHTCPP--CPAPEL 237

Db 200 -LYTLSSSVTVTPSSSQSITCNVAHPASSTKVDKIEPRG-PTIKPCPCPKCPAPNLL 257

Qy 238 GGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNNAKTPREE 297

Db 258 GGPSVFIIPPKDPTLMISLSPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQTHRED 317

Qy 298 YNSTYRVVSVLTVLHQDLNMEKEEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 357

Db 318 YNSTYRVVSVLTVLHQDLNMEKEEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 377

Qy 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDK 417

Db 378 EEMTKQVTLTCHITDFFPEDITVEWQWNGQPENNYKTTPPVLDSDGSFPLYSKLTVDK 437

Qy 418 RWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 449

Db 436 DRNSWQEGDPTTCVMHEALHNHYTQKSLSLSPGK 470

Db 438 NWVERNSYSCSVVHGLHHHTTKFSRTPGK 469

## RESULT 9

S69339  
Ig heavy chain V region precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C:Accession: S69339; S72664  
R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; MUID:95262687; PMID:7744049  
A:Accession: S69339  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <KHA>  
A:Cross-references: EMBL:X81695  
R:Khamilichi, A.A.  
submitted to the EMBL Data Library, September 1994  
A:Reference number: S72664  
A:Accession: S72664  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140, 'C', 142-374 <KH2>  
A:Cross-references: EMBL:X81695  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 46.3%; Score 1423; DB 2; Length 374;  
Best Local Similarity 61.9%; Pred. No. 6.4e-73;  
Matches 281; Conservative 23; Mismatches 46; Indels 104; Gaps 4;

QY	1	EVTLVESGDFVFKPGSLKVS	CAAGFAPSH--YAMSVWRQTPAKRL	EWAYISSGGSGT	58
DB	20	QITLKESGPTLVKQTTLT	LTCTFGSFLSKSGVGVGI	ROPPGQALEWALI-FWDDK	78
QY	59	YVSDSVKGRFTISRDN	AKNTLYLQWRLS	EDSAMVFC	RVKLG---
DB	79	RVSPSLRTRLTITK	DSKQNVLTWNVDP	ADATATYCGY	VEGQGGTFLV 138
QY	116	TVSSASTKGPSVF	LAPSSKSTSGGTA	ALGCLVKDYF	PEPVTVMNSGALTSGVHTPAV 175
DB	139	TVSS-----			----- 142
QY	176	LOSSGLYSLSSVV	VPSSSLGTQYIC	NVNHKPSNTK	VDKVKPEKSCDKTHTCPCPAPE 235
DB	143	-----			-----EPKSCDKTHTCPCPAPE 160
QY	236	LLGGPSVFLFP	PKPDTLMISRTPE	VTVCVVVDVSHED	PEVKFNWVVDGVEVHNATKPRE 295
DB	161	LLGGPSVFLFP	PKPDTLMISRTPE	VTVCVVVDVSHED	PEVKFNWVVDGVEVHNATKPRE 220
QY	296	EQYNSTYRVSV	VLTVLHQDLN	KGKEYCKVSNKAL	PAPIEKTISKAKGQPREPQVYTLPP 355
DB	221	EQYNSTYRVSV	VLTVLHQDLN	KGKEYCKVSNKAL	PAPIEKTISKAKGQPREPQVYTLPP 280
QY	356	SRDELTKNQVSL	TVLVKGFPSDIA	VEWESNGQPENNY	KTTTPVLDSDGSPFLYSKLTVD 415
DB	281	SREEMTKNQVSL	TVLVKGFPSDIA	VEWESNGQPENNY	KTTTPVLDSDGSPFLYSKLTVD 340
QY	416	KSRWQGNVFC	SVMH	EAALHHNYTK	SLSPGK 449
DB	341	KSRWQGNVFC	SVMH	EAALHHNYTK	SLSPGK 374

## RESULT 10

S40295  
Ig gamma-2a chain (mab735) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 09-Jul-2004  
C:Accession: S40295  
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; B  
submitted to the EMBL Data Library, January 1993

A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against  
A:Reference number: S40295  
A:Accession: S40295  
A:Molecule type: protein  
A:Residues: 1-446 <KLE>  
A:Cross-references: UNIPROT:Q99L25  
C:Genetics:

A:Map position: 12  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid  
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>  
F:1-117/Domain: V-D-J region <VDJ>  
F:118-446/Domain: C region <CHR>  
F:118-214/Domain: C1 region <CH1>  
F:215-230/Region: hinge  
F:231-340/Domain: C2 region <CH2>  
F:341-446/Domain: C3 region <CH3>  
F:360-427/Domain: immunoglobulin homology <IMW>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted  
F:132/Disulfide bonds: interchain (to light chain) #status predicted  
F:224,227,229/Disulfide bonds: interchain #status predicted  
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 46.3%; Score 1421; DB 2; Length 446;  
Best Local Similarity 58.7%; Pred. No. 1e-72;  
Matches 264; Conservative 71; Mismatches 109; Indels 6; Gaps 4;

QY	1	EVTLVESGDFVFKPGSLKVS	CAAGFAPSHYAMSVWRQTPAKRL	EWAYISSGGSGTY 60
DB	1	QIQLQSGPELV	RGASVKISCKASGVTFTDYIHWVK	QRPGEGLWGIYPGSGNTKY 60
QY	61	SDSVKGRFTISRDN	AKNTLYLQWRLS	EDSAMVFC
DB	61	NEKFKGATLT	VTDTSSSTAYMQLS	LTSEDSAVYFCARG--GKFAMDYMGQGTSTVTSSA 118
QY	121	STKGPSVFL	LAPSSKSTSGGTA	ALGCLVKDYFPEPVTVMNSGALTSGVHTFP
DB	119	KTTAPSV	FLAPVCGDTTGSSVT	LGCLVKGFPEPVTLTWNSGSLSSGSHVTFPAVLQSD- 177
QY	181	LYSLSSVV	TVPSSSLGTQYIC	NVNHKPSNTKVDKVPKSCDKTHTCPP--CPAP
DB	178	LYTLSSSV	TVTSTWPSQSI	TCNVAHPASSTKVDKIEPRG-PTIKPCPPCKCPAPNLIG 236
QY	239	GPSVFL	PPPKDTLMISRTPE	VTVCVVVDVSHEDPEVKFNWVVDGVEVHNATKPREQY 298
DB	237	GPSVFI	PPPKIDVLMISL	SPMVTVCVVVDVSEDDPDQISWFWANNVEVLTATQTQTHREDY 296
QY	299	NSTYRV	SVSVLTVLHQDLN	KGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 358
DB	297	NSTYRV	SVSVLPIQHD	WMSGKEFKCKVNNKDLPAPIERTISKPGSVRAPQVYVLPPEE 356
QY	359	ELTKNQVSL	TVLVKGFPSDIA	VEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSR 418
DB	357	EMTKQV	TLTLCMTDF	PEPDIYVEWTNNGKTELNYKTEPVLDSGSPFLYSKLAVERKN 416
QY	419	WQGNV	FCSCVM	HEALHHNYTKSLSPG 448
DB	417	WVERNSY	SCSVVH	EGLHHHTTKFSRTPG 446

## RESULT 11

S31459  
Ig gamma-1 chain - sheep (fragment)  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999  
A:Accession: S31459  
R:Patric, S.; Nau, F.  
submitted to the EMBL Data Library, December 1992  
A:Reference number: S31459  
A:Accession: S31459  
A:Status: preliminary  
A:Molecule type: mRNA

A;Residues: 1-472 <PAT>  
A;Cross-references: EMBL:X69797  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;277-346/Domain: immunoglobulin homology <IMM>  
  
Query Match 46.0%; Score 1412; DB 2; Length 472;  
Best Local Similarity 58.4%; Pred. No. 3.5e-72;  
Matches 269; Conservative 66; Mismatches 108; Indels 18; Gaps 5;  
  
QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAPSHYAMSVWROTPAKRLEWVAIYSSGGSG--- 57  
DB 18 QVRLQSGPSLALQLTSLVCTISGFSLNNYGVWVRQAPGKALEWL-----GGSGYDE 72  
  
QY 58 -TYISDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMFYCTRVKJLGTY-----FDSWG 110  
DB 73 DIDYNPVLKSLRSLTKDTSKSQVSLTSLTVTTEDTAVVYCARVDYDSSHAFAYASYDFWG 132  
  
QY 111 QGTTTLTVSSASTGKPSVFPPLAPSKSTSGGTAAALGCLVKDYFPPEPVTVSNWNSGALTSGVH 170  
DB 133 PGLLISVLSASTTPPKYPLTSCCGDTSSSIVTLGCLVSSYMPPEPVTVWNSGALTSGVH 192  
  
QY 171 TFPVAVLQSSGLYSLSSVTVVPSLSLGTQYICNVNHKPSNTKVDKVEPKSCDKTHTCPP 230  
DB 193 TFPVAVLQSSGLYSLSSVTVVPSLSLGTQYICNVNHKPSNTKVDKVEPKSCDKTHTCPP 251  
  
QY 231 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 290  
DB 252 CPPPELPGGPSVFLFPPKPKDTLISGTPEVTCVVDVGDQDDPEVQSFVFNVEVTRAR 311  
  
QY 291 TKPREEQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIETKISKAKGQPREPQV 350  
DB 312 TKPREEQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIETKISKAKGQPREPQV 371  
  
QY 351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNQP--ENNYKTTTPVLDSDGSFEL 408  
DB 372 YVLAAPQEEELKSTLSVTCILVTGYFDYIAVEWKNQGPSSEDKYGTGTTTSQLDADGSYFL 431  
  
QY 409 YSKLTVDKSRWQGNVPSFCVWHEALHNHYTKLSLSLSPGK 449  
DB 432 YSLRLVDRKSNQSGDYIYACVWHEALHNHYTKLSLSPGK 472  
  
RESULT 12  
G2MS11  
IG gamma-2b chain - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1980 #sequence\_revision 01-Dec-2000.#text\_change 09-Jul-2004  
C;Accession: S25057; A02157; A26232; A26233; A53598  
R;Fischer, R.; Voss, A.; Nierbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
submitted to the EMBL Data Library, July 1992  
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m  
A;Reference number: S25057  
A;Accession: S25057  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-474 <PIS>  
A;Cross-references: UNIPROT:P01866; EMBL:X67210; NID:q54826; PIDN:CAA47649.1; PID:q54827  
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.  
Nature 283, 786-789, 1980  
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from r  
A;Reference number: A02157; MUID:90120716; PMID:6766534  
A;Contents: a allele  
A;Accession: A02157  
A;Molecule type: DNA  
A;Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>  
A;Cross-references: GB:J00461  
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
Science 206, 1299-1303, 1979  
A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea  
A;Reference number: A26232; MUID:80081501; PMID:117549  
A;Contents: MPC 11

A;Accession: A26232  
A;Molecule type: mRNA  
A;Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>  
R;Note: Lys-474 is probably removed posttranslationally  
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
Science 206, 1303-1306, 1979  
A;Title: Sequence of the cloned gene for the constant region of murine gamma2b immunogl  
A;Reference number: A26232; MUID:80081502; PMID:117549  
A;Accession: A26232  
A;Molecule type: DNA  
A;Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>  
R;Ollor, R.; Rougeon, F.  
Nature 296, 761-763, 1982  
A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma  
A;Reference number: A26233; MUID:82173203; PMID:6803173  
A;Contents: b allele  
A;Accession: A26233  
A;Molecule type: DNA  
A;Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>  
A;Cross-references: GB:J00461  
R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi  
J. Biol. Chem. 269, 12345-12350, 1994  
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
A;Reference number: A53598; MUID:94216359; PMID:7512967  
A;Accession: A53598  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 234-251 <KIM>  
C;Comment: The a allele sequence is shown.  
C;Genetics:  
A;Intons: 138/1; 236/1; 258/1; 368/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobul  
F;157-222/Domain: immunoglobulin homology <IM>  
F;236-257/Region: hinge  
F;281-350/Domain: immunoglobulin homology <IM2>  
F;387-454/Domain: immunoglobulin homology <IM3>  
F;152/Disulfide bonds: interchain (to light chain) #status predicted  
F;164-220, 288-348, 394-452/Disulfide bonds: #status predicted  
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted  
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted  
  
Query Match 44.4%; Score 1365; DB 1; Length 474;  
Best Local Similarity 55.8%; Pred. No. 1.6e-69;  
Matches 256; Conservative 72; Mismatches 117; Indels 14; Gaps 4;  
  
QY 1 EVTLVESGGDFVKPGGSLKVSAAAGFAPSHYAMSVWROTPAKRLEWVAIYSSGGSGTY 60  
DB 20 EVQLQSGPELVNPGASVMSKASGYTFTYMHVWVKQKPGQGLEWIGVYINPNKDKGTFK 79  
  
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMFYCTRVKJLGTY---YFDSMGQGTTLTV 117  
DB 80 NEKFKGKATLSDKSNSTAYMELSLTSDSAVYICAR---DYDVMFAYWQGGTLTV 135  
  
QY 118 SSAETLKGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 177  
DB 136 SAAKTPSPVPLAPGCGDTTSSVTSGLVKGYFPESVTVWNSGSLSSVHTLQALL 195  
  
QY 178 SGLYSLSSVTVVPSLSLGTQYICNVNHKPSNTKVDKVEPKSCDKT-HTCPP----- 230  
DB 196 QSGLYTMSSSVTVPSSTWPSQTVCVAHPASSTTVTKKLEPSGPISTINPCPECKCHK 255  
  
QY 231 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 290  
DB 256 CPANLEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 315  
  
QY 291 TKPREEQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIETKISKAKGQPREPQV 350  
DB 316 TQTHREDYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIETKISKAKGQPREPQV 375  
  
QY 351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNQPENNYKTTTPVLDSDGSFELYS 410

Db 376 YILPPAQLSKDVSILCLVGFNPGDISVWHTNGHTEENYKDTAPVLSDSGSYFIYS 435  
QY 411 KLTVDKSRWQGNVPSVCSVMHEALHNHYTKSLSLSPGK 449  
Db 436 KLNMTSKWEKTDSPSCNVRHEGLKNYLYLKKTIISRSPGK 474  
RESULT 13  
S01321  
Ig gamma-2b chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 23-Jul-1999  
C:Accession: S01321  
Ride waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.  
Eur. J. Biochem. 176, 287-295, 1988  
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a  
A:Reference number: S01320; MUID:88329081; PMID:3138116  
A:Accession: S01321  
A:Molecule type: mRNA  
A:Residues: 1-475 <Del>  
A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781  
A:Note: this sequence was determined from the differentiated gene  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>  
F:159-223/Domain: immunoglobulin homology <IMM>  
Query Match 43.7%; Score 1343.5; DB 2; Length 475;  
Best Local Similarity 55.4%; Pred. No. 2.5e-68;  
Matches 253; Conservative 75; Mismatches 120; Indels 9; Gaps 4;  
QY 1 EVTLVESGDFVKPGGSLKVS CAASGPAF SHYAMSVRQTAPKRLWAVYISSGSGTY 60  
Db 20 QVOLQSGAELARPGASVKLSCKASGYTLTSYGISWVKQRTQGLEWIGEIVPGSGSYF 79  
QY 61 SDSVKGRTISRDNAKNTLYLQMRSLRSDSNMYECTRVK-LGTYYPDSWGQGTLLTVSS 119  
Db 80 NEKFKGKATLTVDKSSSTAYLHLSLTSEDSAVYFCAGPRQVGLLPFGYWGQGLTVTASA 139  
QY 120 ASTKGPSVFLPAPSSKSTSGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 179  
Db 140 AKTTPSVYPLAPGCGDTTSGSVTLGCLVKGYFPEPTVTSWNSGSLSSVHTFPALLO-S 198  
QY 180 GLYSLSVVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKT-HTCPP-----CP 232  
Db 199 GLYTMSSSVTPSSRWPSQTVCVAHPASSTTVDBKLEPSGPTSTINPCPPCKECHKCP 258  
QY 233 APGLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 292  
Db 259 APNLEGGPSVFIFPPNIKDVLMSLTPTKVTCTVVDVSEDDPDVQISWFNVNVVLTATQ 318  
QY 293 PREEQYNSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPQVY 352  
Db 319 THREDYNSTIRVVSALPTQHQDWMGSKGFECKVKVNNKDLPAPIETISKIGIVRAPQYI 378  
QY 353 LPSPDELTKNQVSTCLVKGYFSPDIAVEWESNQPNENYKTPPVLDSDGSFPLYSKL 412  
Db 379 LSPPEQLSRKDVSLTCLAVGSPEDISVEMTSNGHTSEENYKDTAPVLSDSGSYFIYSKL 438  
QY 413 TVDKSRWQGNVPSVCSVMHEALHNHYTKSLSLSPGK 449  
Db 439 NMKTSKWEKTDSPSCNVRHEGLKNYLYLKKTIISRSPGK 475  
RESULT 14  
I47159  
Ig gamma 2a chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47159  
R,Kacekovic, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47159  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124  
C:Genetics:  
A:Gene: IGG2a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>  
Query Match 41.1%; Score 1263; DB 2; Length 328;  
Best Local Similarity 69.6%; Pred. No. 5.3e-64;  
Matches 231; Conservative 43; Mismatches 52; Indels 6; Gaps 2;  
QY 120 ASTKGPSVFLPAPSSKSTSGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 179  
Db 1 AKTAPSVYPLAPCSRDTSGPNVALGCLASSYFPEPTVTSWNSGSLSSGVHTFPAVLQPS 60  
QY 180 GLYSLSVVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 239  
Db 61 GLYSLSWMTVPASSLSKSYTCNVNHPATTTKVDKRVGTGKTKPPCPICPACESP----G 116  
QY 240 PSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299  
Db 117 PSVFIKPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 176  
QY 300 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPQVYTPPPSDE 359  
Db 177 STYRVSVLPTQHQDWMGSKGFECKVKVNNKDLPAPIETISKAKGQPREPQVYTPPPHAE 236  
QY 360 LTKNQVSLTCLVKGYFSPDIAVEWESNQ--PENNYKTPPVLDSDGSFPLYSKLTVDKS 417  
Db 237 LSRKSVITCLVIGFYPPDIDVEMQRNGQPEPNYRTTPQDQVDGTYFLYKSFSDKA 296  
QY 418 RWQGNVPSVCSVMHEALHNHYTKSLSLSPGK 449  
Db 297 SWQGGIFQCAVMHEALHNHYTKSLSLSPGK 328  
RESULT 15  
S31866  
Ig gamma-1 chain C region - synthetic  
C:Species: synthetic  
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C:Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C:Accession: S31866  
R,Filipula, D.  
submitted to the EMBL Data Library, February 1993  
A:Description: Screening method for protein-protein interactions of cloned gene products.  
A:Reference number: S31866  
A:Accession: S31866  
A:Molecule type: mRNA  
A:Residues: 1-255 <FIL>  
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069  
C:Keywords: immunoglobulin  
F:1-22/Region: Escherichia coli outer membrane protein A precursor  
F:23-255/Region: human Ig gamma-1 chain C region  
Query Match 41.0%; Score 1260; DB 4; Length 255;  
Best Local Similarity 97.5%; Pred. No. 5.8e-64;  
Matches 233; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 211 TKVDKVEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 270  
Db 17 TVAQADVESKSKDTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 76  
QY 271 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHODWLNKGYKCKVSNKAL 330  
Db 77 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHODWLNKGYKCKVSNKAL 136

Qy	331	PAP	IEK	TIS	KAK	Q	P	R	E	P	Q	V	T	L	P	P	S	R	D	E	L	T	K	N	O	V	S	L	T	C	L	V	K	G	F	P	S	D	I	A	V	E	S	N	G	Q	P	E	390							
Db	137	PAP	IEK	TIS	KAK	Q	P	R	E	P	Q	V	T	L	P	P	S	R	D	E	L	T	K	N	O	V	S	L	T	C	L	V	K	G	F	P	S	D	I	A	V	E	S	N	G	Q	P	E	196							
Qy	391	N	N	Y	K	T	T	P	P	V	L	D	S	D	G	S	F	L	Y	S	K	L	T	V	D	K	S	R	W	O	O	G	N	V	F	C	S	V	M	H	E	A	L	N	H	Y	T	O	K	S	L	S	P	G	K	449
Db	197	N	N	Y	K	T	T	P	P	V	L	D	S	D	G	S	F	L	Y	S	K	L	T	V	D	K	S	R	W	O	O	G	N	V	F	C	S	V	M	H	E	A	L	N	H	Y	T	O	K	S	L	S	P	G	K	255

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Job time : 34.9571 secs

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OM protein - protein search, using sw model

Run on: August 1, 2005, 08:49:55 ; Search time 151.023 Seconds  
(without alignments)  
1973.408 Million cell updates/sec

Title: US-10-089-500-57

Perfect score: 3071

Sequence: 1 EVTLVSGGDFVPGSLKV.....IVEFLNRWTFQCSIIISTLT 582

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2184	71.1	470	2 Q6FUA4	Q6pja4 homo sapien
2	2184	71.1	478	2 Q6PI81	Q6pi81 homo sapien
3	2166.5	70.5	475	2 Q6MZQ6	Q6mzq6 homo sapien
4	2160	70.3	472	2 Q6N089	Q6n089 homo sapien
5	2157.5	70.3	475	2 Q6GMW7	Q6gmw7 homo sapien
6	2152.5	70.1	473	2 Q6MZV7	Q6mzv7 homo sapien
7	2146	69.9	480	2 Q6N094	Q6n094 homo sapien
8	2145	69.7	544	2 Q6PJ95	Q6pj95 homo sapien
9	2140.5	69.7	544	2 Q6N096	Q6n096 homo sapien
10	2126	69.2	466	2 Q6N095	Q6p055 homo sapien
11	2124.5	69.2	473	2 Q6P055	Q6p055 homo sapien
12	2124	69.2	470	2 Q7Z5W1	Q7z5w1 homo sapien
13	2111	68.7	482	2 Q7Z351	Q7z351 homo sapien
14	2080.5	67.7	481	2 Q6N097	Q6n097 homo sapien
15	2066.5	67.3	469	2 Q7Z7P5	Q7z7p5 homo sapien
16	2052.5	66.8	475	2 Q6N095	Q6n095 homo sapien
17	2037	66.3	476	2 Q6GMX1	Q6gmx1 homo sapien
18	2027.5	66.0	465	2 Q6GMX6	Q6gmx6 homo sapien
19	2026	66.0	480	2 Q6PJF1	Q6pjf1 homo sapien
20	2018.5	65.7	465	2 Q6P6C4	Q6p6c4 homo sapien
21	2014	65.6	464	2 Q6MZU6	Q6mzu6 homo sapien
22	1957.5	63.7	521	2 Q8N4Y9	Q8n4y9 homo sapien
23	1956	63.7	518	2 Q6N030	Q6n030 homo sapien
24	1939	63.1	493	2 Q68CN4	Q68cn4 homo sapien
25	1916	62.4	417	2 Q6N093	Q6n093 homo sapien
26	1824	59.4	348	2 Q6PYX1	Q6pyx1 homo sapien
27	1812	59.0	473	2 Q8TC63	Q8tc63 homo sapien
28	1790.5	58.3	476	2 Q6MZX7	Q6mzx7 homo sapien
29	1767	57.5	330	1 GC1_HUMAN	P01857 homo sapien
30	1622.5	52.8	509	2 Q8NF17	Q8nf17 homo sapien
31	1604	52.2	326	1 GC2_HUMAN	P01859 homo sapien

32	1590.5	51.8	327	1 GC4_HUMAN	P01861 homo sapien
33	1535.5	50.0	487	2 Q65ZL2	Q65zl2 mus ap. fv/
34	1527.5	49.7	473	2 Q91Z05	Q91z05 mus musculu
35	1524.5	49.6	354	2 Q86TT2	Q86tt2 homo sapien
36	1521.5	49.5	471	2 Q68K04	Q68k04 mus musculu
37	1509	49.1	458	2 Q65ZQ1	Q65zq1 homo sapien
38	1484	48.3	464	2 Q6FIP8	Q6fip8 mus musculu
39	1456.5	47.4	473	2 Q9D8L4	Q9d8l4 mus musculu
40	1455.5	47.4	463	2 Q99LC4	Q99lc4 mus musculu
41	1454	47.3	470	2 Q7TMK1	Q7tmk1 mus musculu
42	1447	47.1	472	2 Q6PJ47	Q6pj47 mus musculu
43	1442.5	47.0	465	2 Q6FJB2	Q6fjb2 mus musculu
44	1419	46.2	464	2 Q6PF95	Q6pf95 mus musculu
45	1399	45.6	474	2 Q8R3H6	Q8r3h6 mus musculu
46	1266.5	41.2	337	2 Q95M34	Q95m34 equus cabal
47	1264	41.2	679	2 Q96P08	Q96p08 homo sapien
48	1230.5	40.1	323	1 GC_RABIT	P01670 oryctolagus
49	1216.5	39.6	329	1 GC3_CAVPO	P01862 cavia porce
50	1156	37.6	290	1 GC1_HUMAN	P01860 homo sapien
51	1152	37.5	326	1 GCI_RAT	P20759 rattus norv
52	1146.5	37.3	333	1 GCB_RAT	P20761 rattus norv
53	1142	37.2	324	1 GCI_MOUSE	P01868 mus musculu
54	1141	37.2	329	1 GC1_MOUSE	P22436 mus musculu
55	1139	37.1	393	1 GC1M_MOUSE	P01869 mus musculu
56	1130	36.8	398	1 GC3M_MOUSE	P03387 mus musculu
57	1126	36.7	330	1 GCAA_MOUSE	P01863 mus musculu
58	1123.5	36.6	335	1 GCAB_MOUSE	P01864 mus musculu
59	1121	36.5	399	1 GCAM_MOUSE	P01865 mus musculu
60	1118.5	36.4	329	1 GCC_RAT	P20762 rattus norv
61	1112	36.2	322	1 GCA_RAT	P20760 rattus norv
62	1087	35.4	336	1 GCB_MOUSE	P01866 mus musculu
63	1082	35.2	405	1 GC8M_MOUSE	P01867 mus musculu
64	877.5	28.6	606	2 Q6GMV2	Q6gmv2 homo sapien
65	856	27.9	597	2 Q66BB9	Q66bb9 homo sapien
66	849.5	27.7	584	2 Q6LHK3	Q6lkh3 xenopus lae
67	847	27.6	613	2 Q8WUK1	Q8wuk1 homo sapien
68	842	27.4	487	2 Q99KA4	Q99ka4 mus musculu
69	834.5	27.2	303	2 Q6KAM2	Q6kam2 mus musculu
70	828.5	27.0	486	2 Q91Z07	Q91z07 mus musculu
71	816	26.6	585	2 Q6GXP4	Q6gxp4 xenopus lae
72	807	26.3	479	2 Q91WP5	Q91wp5 mus musculu
73	799	26.0	493	2 Q6GMX2	Q6gmx2 homo sapien
74	793.5	25.8	494	2 Q66K68	Q66k68 homo sapien
75	788	25.7	593	2 Q6INM5	Q6inm5 xenopus lae
76	787	25.6	614	2 Q6DDQ7	Q6ddq7 xenopus lae
77	785	25.6	480	2 Q91XE1	Q91xe1 mus musculu
78	783	25.5	485	2 Q6PDB8	Q6pdb8 mus musculu
79	781	25.4	499	2 Q8N5K4	Q8n5k4 homo sapien
80	776	25.3	493	2 Q8NCL6	Q8nc16 homo sapien
81	772	25.1	479	2 Q6MZV6	Q6mzv6 homo sapien
82	768	25.0	487	2 Q6ZVX0	Q6zvx0 homo sapien
83	753.5	24.5	494	2 Q8ZM64	Q8zm64 homo sapien
84	749	24.4	483	2 Q6MZX9	Q6mzx9 homo sapien
85	748.5	24.4	484	2 Q8VEA0	Q8vea0 mus musculu
86	748	24.4	487	2 Q80Z17	Q80z17 mus musculu
87	747	24.3	613	2 Q8VCX7	Q8vcx7 mus musculu
88	737	24.0	519	2 Q6N092	Q6n092 homo sapien
89	731.5	23.8	614	2 Q7TMT6	Q7tmt6 mus musculu
90	709	23.1	597	2 Q6GMX5	Q6gmx5 homo sapien
91	709	23.1	597	2 Q9BU10	Q9bu10 homo sapien
92	703	22.9	498	2 Q6N041	Q6n041 homo sapien
93	703	22.9	597	2 Q8BQB8	Q8bqb8 homo sapien
94	697.5	22.7	595	2 Q8WUX4	Q8wux4 homo sapien
95	697.5	22.7	625	2 Q96AA6	Q96aa6 homo sapien
96	690.5	22.5	500	2 Q6N091	Q6n091 homo sapien
97	690	22.5	153	1 IL2_HUMAN	P60568 homo sapien
98	690	22.5	153	1 IL2_HYLLA	P60569 hylobates l
99	690	22.5	153	2 Q6NZ93	Q6n293 homo sapien
100	687.5	22.4	500	2 Q9BRV0	Q9brv0 homo sapien

ALIGNMENTS

```
RESULT 1
Q6FJA4 PRELIMINARY; PRT; 470 AA.
AC Q6FJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RC SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RX Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
RL EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; 1AQQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig C1.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match
Best Local Similarity 91.4%; Score 2184; DB 2; Length 470;
Matches 412; Conservative 10; Mismatches 27; Indels 2; Gaps 1;

QY 1 EVTLVESGDFVYKPGSLKVCASGAPFASHYMSWVRQTAKRLWVAYISGSGSGTY 60
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 EVQLVESGGLVQPGSLRLSCVSGFTFSSYMSWVRQAPGKLEWVANIQQDSEK 79
QY 61 SDSVKGRTISRDNAKNTLYLQMRSLRSDSNMYECTRVKLTGY--YDSWCGQTLTVS 118
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 VDSVKGRTISRDNAKNTLYLQMRSLRSDSNMYECTRVKLTGY--YDSWCGQTLTVS 139
QY 119 SASTKGPSVFPPLAPSSKTSKSTGTAALGCLVKDYFPPEPTVTSWNSGALTSVHTFPVLIQS 178
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
140 SASTKGPSVFPPLAPSSKTSKSTGTAALGCLVKDYFPPEPTVTSWNSGALTSVHTFPVLIQS 199
```



DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 71.1%; Score 2184; DB 2; Length 478;  
Best Local Similarity 90.0%; Pred. No. 1.2e-131;  
Matches 413; Conservative 13; Mismatches 23; Indels 10; Gaps 2;

QY 1 EVTLVESGGDFVKPGGSLKVSACAASGPAFSHYAMSVNRQTPAKRLEWVAYISSGSGTY 60  
DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMVNRQAPKGLEWVANI KQDSEKYY 79  
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTR-----VKLGTYF--DSWG 110  
DB 80 VDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTR-----VKLGTYF--DSWG 139  
QY 111 QGTTLVSSASTKGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVH 170  
DB 140 KGTITVTSSASTKGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVH 199  
QY 171 TFAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKSNKTKVDPKPKCDKTHTCPP 230  
DB 200 TFAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKSNKTKVDPKPKCDKTHTCPP 259  
QY 231 CPAPELLGGPSVFLPAPSKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 290  
DB 260 CPAPELLGGPSVFLPAPSKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 319  
QY 291 TKPREQYNSTYRVVSVLTVLHQDLMLGKEYCKVSNKALPAPIEKTISKAKGQPREPQV 350  
DB 320 TKPREQYNSTYRVVSVLTVLHQDLMLGKEYCKVSNKALPAPIEKTISKAKGQPREPQV 379  
QY 351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 410  
DB 380 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 439  
QY 411 KLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK 449  
DB 440 KLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK 478

RESULT 3  
Q6MZQ6 PRELIMINARY; PRT; 475 AA.

ID Q6MZQ6 PRELIMINARY; PRT; 475 AA.  
AC Q6MZQ6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp666G11190.  
GN Names=DKFZp666G11190;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human esophagus tumor;  
RG The German Human cDNA Consortium;  
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640947; CAE45972.1; -.  
DR HSSP; P01861; 1ADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.

DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 70.5%; Score 2166.5; DB 2; Length 475;  
Best Local Similarity 89.0%; Pred. No. 1.6e-130;  
Matches 406; Conservative 18; Mismatches 25; Indels 7; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVSACAASGPAFSHYAMSVNRQTPAKRLEWVAYISSGSGTY 60  
DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFRNYYAMNVRQAPKGLEWVSGISSGVNTYY 79  
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRVKLGTY-----YFDSWGOGT 113  
DB 80 ADSVKGRFTISGDISTNTLYLQMRSLRADDTAVYYCARADYRDYQVSPAYWYFDVWGRGT 139  
QY 114 TLTVSSASTKGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFP 173  
DB 140 LVSVSAASTKGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFP 199  
QY 174 AVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKSNKTKVDPKPKCDKTHTCPPCPA 233  
DB 200 AVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKSNKTKVDPKPKCDKTHTCPPCPA 259  
QY 234 PELLGGPSVFLPAPSKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 293  
DB 260 PELLGGPSVFLPAPSKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319  
QY 294 REEQYNSTYRVVSVLTVLHQDLMLGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 353  
DB 320 REEQYNSTYRVVSVLTVLHQDLMLGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379  
QY 354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 413  
DB 380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 439  
QY 414 VDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK 449  
DB 440 VDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK 475

RESULT 4  
Q6N089 PRELIMINARY; PRT; 472 AA.

ID Q6N089 PRELIMINARY; PRT; 472 AA.  
AC Q6N089;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp666P15220.  
GN Names=DKFZp666P15220;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RG The German Human cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640627; CAE45781.1; -.  
DR HSSP; P01861; 1ADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.



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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RG The German Human cDNA Consortium;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAB45920.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 3.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 9476BAE4C0BF447 CRC64;

Query Match 70.1%; Score 2152.5; DB 2; Length 473;
Best Local Similarity 88.3%; Pred. No. 1.3e-129;
Matches 40; Conservative 24; Mismatches 24; Indels 5; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVSACASGFAPFASHYAMSVWROTPAKRLWVAVYISSGGSGTY 60
DB 20 EIQLVESGGGLVQPGGSLRLSCLASGFTFSFENNWVRQAPGKLEWLSVITRSGNTVY 79

QY 61 SDSVKGRTISRDNANKTLYLQMRSLRSDSAMYFCTRVKLT-----YTFDSNGQTTL 115
DB 80 ADSLQGRFTISRDNARNSLYLQMNLSRAEDTAVYICARQNEHTSPWYPSFDYMGQGLV 139

QY 116 TVSSASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAV 175
DB 140 TVSSASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFLEPTVSWNSGALTSGVHTTTPAV 199

QY 176 LQSSGLYSLSSVTVPSSSSLGTQTYICNVNHPKSNKVDKVPKSCDKHTHTCCPAPE 235
DB 200 LQSSGLYSLSSVTVPSSSSLGTQTYICNVNHPKSNKVDKVPKSCDKHTHTCCPAPE 259

QY 236 LLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPRE 295
DB 260 LLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPRE 319

QY 296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTTISKAGQPRQPQVYTLPP 355
DB 320 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTTISKAGQPRQPQVYTLPP 379

QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVD 415
DB 380 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVD 439

QY 416 KSRWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 449
DB 440 KSRWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 473

RESULT 7
Q6N094
ID Q6N094 PRELIMINARY; PRT; 480 AA.
AC Q6N094;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKF2p686O01196.
GN Name=DKF2p686O01196;
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640822; CAB45776.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 3.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;

Query Match 69.9%; Score 2146; DB 2; Length 480;
Best Local Similarity 87.4%; Pred. No. 3.3e-129;
Matches 40; Conservative 19; Mismatches 27; Indels 12; Gaps 1;

QY 1 EVTLVESGGDFVKPGGSLKVSACASGFAPFASHYAMSVWROTPAKRLWVAVYISSGGSGTY 60
DB 20 EEELVESGGGLVKPGGSLRLSCLASGFTFSFENNWVRQAPGKLEWLSVITRSGNEKY 79

QY 61 SDSVKGRTISRDNANKTLYLQMRSLRSDSAMYFCTRVK-----LGTYYFDS 108
DB 80 GESVKGRTISRDNADNSLFLQMSLRVDVTATYYCARGKWVPAGPTSTSGPVRHNWFD 139

QY 109 WGGTTLTVSSASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSG 168
DB 140 WGGTTLTVSSASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSG 199

QY 169 VHTFPAVLQSSGLYSLSSVTVPSSSSLGTQTYICNVNHPKSNKVDKVPKSCDKHTHTC 228
DB 200 VHTFPAVLQSSGLYSLSSVTVPSSSSLGTQTYICNVNHPKSNKVDKVPKSCDKHTHTC 259

QY 229 PPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 288
DB 260 PPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 319

QY 289 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTTISKAGQPRP 348
DB 320 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTTISKAGQPRP 379

QY 349 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFL 408
DB 380 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFL 439

QY 409 YSKLTVDKSRWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 449
DB 440 YSKLTVDKSRWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 480

RESULT 8
Q6IN78
ID Q6IN78 PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
GN Name=IGHG1;
```

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -.
DR HSSP; P01861; 1ADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; Igc1; 3.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS0835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0CEDE81076E CRC64;

Query Match 69.8%; Score 2145; DB 2; Length 466;
Best Local Similarity 90.0%; Pred. No. 3.7e-129;
Matches 406; Conservative 15; Mismatches 24; Indels 6; Gaps 3;

QY 1 EVTLVESGGDFVKPGSLKVSACAAGFAPSHYAMSVRQTAPKRLWNAVYISSGGSGTY 60
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
20 EVQLVESGGLIQPGSGSLTSCAASGLTVSSNVMHWVRQAPGKLEWVSLYIGCA-TY 78
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 SDSVKGRTISRDNAKNTLYLQWRSLSRSDSAMYFCTRVKLTGYTPDS--WQGGTTLTV 118
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
79 ADSVKGRTISRDNSKNTLYLQWNSLRDAEDTAVYCAR---GNYYVPAAPWGQGLTVTV 135
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 119 SASTGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 178
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
136 SASTGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 195
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 179 SGLYSLSSVTVTPSSSLGQTQYICNVNKPSTNKVDKVKPEKSCDKHTCCPCPAPELLG 238
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
196 SGLYSLSSVTVTPSSSLGQTQYICNVNKPSTNKVDKVKPEKSCDKHTCCPCPAPELLG 255
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 239 GPSVFLFPKPKDITLMISTPTEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 298
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
256 GPSVFLFPKPKDITLMISTPTEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 315
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 299 NSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIETKISKAGQPREPVVITLPPSRD 358
```

```
DB 316 NSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIETKISKAGQPREPVVITLPPSRD 375
QY 359 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFYLKSLYVDKSR 418
DB 376 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFYLKSLYVDKSR 435
QY 419 WOQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
DB 436 WOQGNVFSCSVMHEALHNHYTQKSLSLSPGK 466
RESULT 9
Q6PJ95 PRELIMINARY; PRT; 544 AA.
ID Q6PJ95
AC Q6PJ95;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019046; AAH19046.1; -.
DR HSSP; P01861; 1ADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; Igc1; 3.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS0835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 544 AA; 1895814B2297C668 CRC64;

Query Match 69.7%; Score 2140.5; DB 2; Length 544;
Best Local Similarity 85.6%; Pred. No. 8.9e-129;
Matches 409; Conservative 16; Mismatches 34; Indels 19; Gaps 2;
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Qy 1 EVTLVESGGDFVVKPGGSLKLVSCAASGFAPFASHYAMSVWRQTPAKLEWVAYISSGGSGTTY 60
D 20 QAQVLVESGGGVVQPGSSLRSLSCAASGFRFNYGMHVWRQAPKGLWVAVFSYDESCKYY 79
Qy 61 SDSVKGRFTTISRDNKNTLYLQMSLSASDSAMFYCTRVKLGTY-----YFDSWGQGT 113
D 80 AASVKGRFTTISRDNKNTLYLQMSLSRVEDTAVYYCAKQKQKQKQKQKQKQKQKQKQKQKQK 139
Qy 114 TLTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFP 173
D 140 LVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFP 199
Qy 174 AVLOSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHCPCPA 233
D 200 AVLOSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHCPCPA 259
Qy 234 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKP 293
D 260 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKP 319
Qy 294 REEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 353
D 320 REEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379
Qy 354 PPSRDELTKQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTPVLDSDGSFELYSLKT 413
D 380 PPSRDELTKQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTPVLDSDGSFELYSLKT 439
Qy 414 VDKSRWQGNVFCVSMVHEALHNHYTQKSLSLSPGKAPTSSSTKTKTQLEHLLDLQ 471
D 440 VDKSRWQGNVFCVSMVHEALHNHYTQKSLSLSPGKAPTSSSTKTKTQLEHLLDLQ 485
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## RESULT 10

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Q6N096 PRELIMINARY; PRT; 466 AA.
AC Q6N096;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686i15196;
GN Name=DKFZp686i15196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weill B., Amid C., Oeinger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640620; CAB45774.1;
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 466 AA; 50926 MW; 01E91B748D6D57C4 CRC64;
```

Query Match 69.2%; Score 2126; DB 2; Length 466;  
Best Local Similarity 89.3%; Pred. No. 6.1e-128;  
Matches 401; Conservative 17; Mismatches 29; Indels 2; Gaps 1;

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Qy 1 EVTLVESGGDFVVKPGGSLKLVSCAASGFAPFASHYAMSVWRQTPAKLEWVAYISSGGSGTTY 60
D 20 QAQVLVESGGGVVQPGSSLRSLSCAASGFRFNYGMHVWRQAPKGLWVAVFSYDESCKYY 79
Qy 61 SDSVKGRFTTISRDNKNTLYLQMSLSASDSAMFYCTRVKLGTY-----YFDSWGQGT 120
D 80 AASVKGRFTTISRDNKNTLYLQMSLSRVEDTAVYYCAKQKQKQKQKQKQKQKQKQKQKQKQK 137
Qy 121 STKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPVAVLOSSG 180
D 138 STKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPVAVLOSSG 197
Qy 181 LYSLSVTVTVVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHCPAPELGGP 240
D 198 LYSLSVTVTVVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHCPAPELGGP 257
Qy 241 SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKPREQYNS 300
D 258 SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKPREQYNS 317
Qy 301 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
D 318 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 377
Qy 361 TKQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTPVLDSDGSFELYSLKTIVDKSRWQ 420
D 378 TKQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTPVLDSDGSFELYSLKTIVDKSRWQ 437
Qy 421 QGNVFCVSMVHEALHNHYTQKSLSLSPGK 449
D 438 QGNVFCVSMVHEALHNHYTQKSLSLSPGK 466
```

RESULT 11

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Q6P055 PRELIMINARY; PRT; 473 AA.
AC Q6P055;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RG MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
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Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

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RA EMBL; BC065820; AAH65820.1; -.
RA HSSP; P01861; IADQ.
DR InterPro; IPR003559; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00407; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ
SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match          69.2%; Score 2124.5; DB 2; Length 473;
Best Local Similarity 88.5%; Pred. No. 7,8e-128;
Matches 402; Conservative 14; Mismatches 33; Indels 5; Gaps 2;

QY 1 EYTLVESGGDFVKPGGSLKVCAGGFAPSHYAMSVRQTPAKRLIEWAYISS--GGSGT 58
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 20 EAHLVESGGGLVRPGGSLTSLTSGSGFTSGAWLSWVRQAPGKLEWVARIQTEDDGGTT 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 59 YISDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVLKGTYYY---YFDSNGGGTTL 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 HYGIAGKGRFTVSRDSDSRNTLYLQMSLDLRTDFAFYFCATGSMNTVGLTGPDSWGGGTLLV 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSVNSGALTSGVHTFPAV 175
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 140 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSVNSGALTSGVHTFPAV 199
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 176 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHKTPCPPAPE 235
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 200 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHKTPCPPAPE 259
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 236 LLGGPSVFLPFPKPKDITLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 295
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 260 LLGGPSVFLPFPKPKDITLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 319
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 296 EQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTIISKAKGPREPQVYTLPP 355
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 320 EQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTIISKAKGPREPQVYTLPP 379
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSFPLYSKLTVD 415
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 380 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSFPLYSKLTVD 439
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 416 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 440 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 473
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
QY25W1 PRELIMINARY; PRT; 470 AA.
AC QY25W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAH53984.1; -.
DR HSSP; P01857; 1H2H.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ
SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match          69.2%; Score 2124; DB 2; Length 470;
Best Local Similarity 89.0%; Pred. No. 8,3e-128;
Matches 404; Conservative 15; Mismatches 27; Indels 8; Gaps 3;

QY 1 EYTLVESGGDFVKPGGSLKVCAGGFAPSHYAMSVRQTPAKRLIEWAYISSGGSGTYY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 20 EVQLVESGGGLVQPGGSLRLSCVASFGLNNYDMHWVRQGIKGLIEWSKIGTAGD-RYY 78
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTR-----VKLGYTFDSWGGTTL 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 79 AGSVKGRFTISRDNKNTLYLQMSLRVGDAAVYICARGAGRWAPLGA--FDIWQGGTAV 136
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSVNSGALTSGVHTFPAV 175
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 137 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSVNSGALTSGVHTFPAV 196
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 176 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHKTPCPPAPE 235
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 197 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHKTPCPPAPE 256
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 236 LLGGPSVFLPFPKPKDITLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 295
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 257 LLGGPSVFLPFPKPKDITLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 316
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 296 EQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTIISKAKGPREPQVYTLPP 355
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 317 EQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTIISKAKGPREPQVYTLPP 376
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSFPLYSKLTVD 415
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 377 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSFPLYSKLTVD 436
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 416 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 437 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
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